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83383

From: Slobodyansky, Elizabeth
Sent: Tuesday, December 31, 2002 12:39 PM
To: STIC-Biotech/ChemLib
Subject: 09/873,075

Please search for case 09/873,075:

21

SEQ ID NO: 1 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652
CM1 10D11
703-306-3222

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Point of Contact:
Mona Smith
Technical Information Specialist
CM1 6A01
Tel: 308-3278

CRT

Searcher: H. Smith
Phone: _____
Location: _____
Date Picked Up: 1/2/3
Date Completed: 1/3/5
Searcher Prep/Review: 5
Clerical: _____
Online time: 4

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

10/1/2010
10/1/2010
10/1/2010
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10/1/2010

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2003, 15:04:44 : Search time 15 Seconds
(without alignments)
380.536 Million cell updates/sec

Title: US-09-873-075A-1
Perfect score: 999
Sequence: 1 QLGAIENGLESGSANACPDPA.....SYTIEARGEARFLDRIRRA 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUTS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	999	100.0	229	2	US-08-817-997A-2
2	500.5	50.1	231	4	US-09-177-234-3
3	499.5	50.0	232	4	US-09-177-234-8
4	482	48.2	232	4	US-09-177-234-6
5	145	14.5	285	4	US-09-095-855-197
6	145	14.5	285	4	US-09-205-426-197
7	119	11.9	748	2	US-08-997-080-154
8	119	11.9	748	2	US-08-997-362-154
9	119	11.9	748	4	US-09-095-855-154
10	119	11.9	748	4	US-09-324-542-154
11	119	11.9	748	4	US-09-205-426-154
12	116	11.6	167	2	US-08-997-080-112
13	116	11.6	167	2	US-08-997-362-112
14	116	11.6	167	4	US-09-095-855-112
15	116	11.6	167	4	US-09-324-542-112
16	116	11.6	167	4	US-09-205-426-112
17	114.5	11.5	28	2	US-08-817-997A-3
18	90	9.0	4550	2	US-08-804-227C-8
19	90	9.0	4550	2	US-08-804-198-2
20	89	8.9	345	2	US-08-282-197C-50
21	89	8.9	592	1	US-08-217-327-8
22	86.5	8.7	200	4	US-09-355-166-18
23	76.5	7.7	1039	4	US-09-409-648-7
24	76.5	7.7	1039	4	US-09-409-648-8
25	76.5	7.7	1039	6	5196511-2
26	76	7.6	414	4	US-09-647-540A-6
27	76	7.6	428	2	US-08-657-641-6

28	76	7.6	428	5	PCT-US94-07233-6	Sequence 6, Appli
29	75.5	7.6	224	1	US-08-707-793A-6	Sequence 6, Appli
30	75.5	7.6	224	1	US-08-707-792A-6	Sequence 6, Appli
31	73.5	7.4	1056	2	US-08-627-873-7	Sequence 7, Appli
32	73	7.3	1451	1	US-08-308-872B-4	Sequence 4, Appli
33	73	7.3	1453	1	US-08-308-872B-6	Sequence 6, Appli
34	73	7.3	1454	4	US-08-392-459-22	Sequence 22, Appli
35	73	7.3	1454	4	US-08-392-459-26	Sequence 26, Appli
36	73	7.3	1454	5	PCT-US91-08525-22	Sequence 22, Appli
37	73	7.3	1454	5	PCT-US91-08525-26	Sequence 26, Appli
38	73	7.3	1454	5	PCT-US93-04384-2	Sequence 2, Appli
39	73	7.3	1454	5	PCT-US93-04384-16	Sequence 16, Appli
40	73	7.3	1454	5	PCT-US93-04384-43	Sequence 43, Appli
41	73	7.3	1454	5	PCT-US93-04384-45	Sequence 45, Appli
42	73	7.3	1454	5	PCT-US93-04384-48	Sequence 48, Appli
43	73	7.3	639	4	US-09-509-814A-4	Sequence 4, Appli
44	72.5	7.2	496	4	US-09-142-481-2	Sequence 2, Appli
45	72					

ALIGNMENTS

RESULT 1
US-08-817-997A-2
: Sequence 2, Application US/08817997A
: Patent No. 5827719
: GENERAL INFORMATION:
: APPLICANT: Sandal, Thomas
: APPLICANT: Kauppinen, Sakari
: APPLICANT: Kofod, Lene V.
: TITLE OF INVENTION: An Enzyme With Lipolytic
: TITLE OF INVENTION: Activity
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 58277190 No. 5827719disk Of No. 5827719th America, Inc.
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10174
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/817,997A
: FILING DATE: 24-APR-1997
: CLASSIFICATION: 7435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4316.204
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-878-9652
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 229 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
US-08-817-997A-2

Query Match 100.0%; Score 999; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 9.7e-107;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGIVGVPALANGLESIRNIWIOGVG 60
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Db 36 OLGAIEENGLESSANACPDAILIFARGSTPEGMGTTVGPALANGLESHIRNIWIOGVGG 95
QY 61 PYDAALATNFPRTGTSQANIDEKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELSG 120
Db 96 PYDAALATNFPRTGTSQANIDEKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELSG 155
QY 121 AVKEQKGVALFGYTONLQNRGIPNPRRTKVFNCVGDVCTGTLITPAHLSYTI EA 180
Db 156 AVKEQKGVALFGYTONLQNRGIPNPRRTKVFNCVGDVCTGTLITPAHLSYTI EA 215
QY 181 RGEAAREFLDRDRI 194
Db 216 RGEAAREFLDRDRI 229

RESULT 2
US-09-177-234-3
; Sequence 3, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Gliocladium sp.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-09-177-234-3

Query Match 50.1%; Score 500.5; DB 4; Length 231;
Best Local Similarity 50.0%; Pred. NO. 1.8e-49;
Matches 95; Conservative 34; Mismatches 58; Indels 3; Gaps 2;

QY 5 IENGLESGSANACPDAILIFARGSTPEGMGTTVGPALANGLESIRNIWIOGVGGPY 62
Db 42 VDELRNG-GSACPRAILIFARGTMELDNMGLLVGPALAGLEGILGSNNLWVQGVGGY 100
QY 63 DAALATNFPRTGTSQANIDEKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELSGAV 122
Db 101 AANLEGNLFPDGTTPKAQEMLSLLQLADTKCPNSKIYTVGGYSOGAALVAAAIRDVKASI 160
QY 123 KEQKGVALFGYTONLQNRGIPNPRRTKVFNCVGDVCTGTLITPAHLSYTI EA 182
Db 161 RQKIVGTVLFGYTRKNQKQGVENYSTDRLRYNCNAGDLICQGTLLVLPALHLYGVQAAG 220
QY 183 EAAREFLDRDI 192
Db 221 PAAQFLASKI 230

RESULT 3
US-09-177-234-8
; Sequence 8, Application US/09177234A
; Patent No. 6350604
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; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Trichophaea saccata
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-09-177-234-8

Query Match 50.0%; Score 499.5; DB 4; Length 232;
Best Local Similarity 50.5%; Pred. NO. 2.3e-49;
Matches 96; Conservative 32; Mismatches 59; Indels 3; Gaps 2;

QY 5 IENGLESGSANACPDAILIFARGSTPEGMGTTVGPALANGLESIRNIWIOGVGGPY 62
Db 42 VDELRNG-GGACPKAILIFARGTMELDNMGLLVGPALAGLEGILGSNNLWVQGVGGY 100
QY 63 DAALATNFPRTGTSQANIDEKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELSGAV 122
Db 101 AANLEGNLFPDGTTPKAQEMLSLLQLADTKCPNSKIYTVGGYSOGAALVAAAIRDVKASI 160
QY 123 KEQKGVALFGYTONLQNRGIPNPRRTKVFNCVGDVCTGTLITPAHLSYTI EA 182
Db 161 RQKIVGTVLFGYTRKNQKQGVENYSTDRLRYNCNAGDLICQGTLLVLPALHLYGVQAAG 220
QY 183 EAAREFLDRDI 192
Db 221 PAAQFLASKI 230

RESULT 4
US-09-177-234-6
; Sequence 6, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
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Db 132 RPLGRFTPTMPRVADHVAVVVFNPLRDIRGGPLQMSGTGPKSKIDCALDDPFC 191

Qy 164 TGTLLITPAHLSYT---IEARGEARTLR 189

Db 192 SPGFNL-PAHFAYADNGWVE---EARNFAR 217

RESULT 7

US-08-997-080-154

; Sequence 154, Application US/08997080

; Patent No. 5968524

; GENERAL INFORMATION:

; APPLICANT: WATSON, JAMES D.

; APPLICANT: TAN, PAUL L.J.

; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-

; NUMBER OF SEQUENCES: 194

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA: US/08/997,080

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-269-0565

; TELEFAX: 206-269-0563

; TELEX:

; INFORMATION FOR SEQ ID NO: 154:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 748 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-997-080-154

Query Match 11.9%; Score 119; DB 2; Length 748;

Best Local Similarity 31.1%; Pred. No. 6.7e-05;

Matches 51; Conservative 21; Mismatches 52; Indels 40; Gaps 12;

Qy 9 LESSGANACPDAILIFARGST-TEPGNMGITVGPALANGLESIRNIWTQGGPYDAALA 67

Db 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVG---QSVG-----TYA 76

Qy 68 TNF-----LPRGTQANIDEGKRLFALANQKCPNTPVVGYSOGAALIAAAV--- 115

Db 77 VNPAGFDKSPMPGAADAS---GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131

Qy 116 -----SELGAVKEQVKGFALFGYTONLON--RGGIPNY-PR 149

Db 132 RPLGRFTPTMPRVADHVAVVVFN--NPLRDIRGGPRLPR 173

Qy 132 RPLGRFTPTMPRVADHVAVVVFN--NPLRDIRGGPRLPR 173

RESULT 8

US-08-997-362-154

; Sequence 154, Application US/08997362

; Patent No. 5985287

; GENERAL INFORMATION:

; APPLICANT: WATSON, JAMES D.

; APPLICANT: TAN, PAUL L.J.

; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF MYCOBACTERIAL INFECTIONS

; NUMBER OF SEQUENCES: 194

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA: US/08/997,362

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1002c2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-269-0565

; TELEFAX: 206-269-0563

; TELEX:

; INFORMATION FOR SEQ ID NO: 154:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 748 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-997-362-154

Query Match 11.9%; Score 119; DB 2; Length 748;

Best Local Similarity 31.1%; Pred. No. 6.7e-05;

Matches 51; Conservative 21; Mismatches 52; Indels 40; Gaps 12;

Qy 9 LESSGANACPDAILIFARGST-TEPGNMGITVGPALANGLESIRNIWTQGGPYDAALA 67

Db 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVG---QSVG-----TYA 76

Qy 68 TNF-----LPRGTQANIDEGKRLFALANQKCPNTPVVGYSOGAALIAAAV--- 115

Db 77 VNPAGFDKSPMPGAADAS---GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131

Qy 116 -----SELGAVKEQVKGFALFGYTONLON--RGGIPNY-PR 149

Db 132 RPLGRFTPTMPRVADHVAVVVFN--NPLRDIRGGPRLPR 173

Qy 132 RPLGRFTPTMPRVADHVAVVVFN--NPLRDIRGGPRLPR 173

RESULT 9

US-09-095-855-154

; Sequence 154, Application US/09095855

; Patent No. 6160093

; GENERAL INFORMATION:

; APPLICANT: TAN, PAUL

; APPLICANT: VISSEER, ELIZABETH

; APPLICANT: SKINNER, MARGOT

; APPLICANT: PRESTIDGE, ROSS

; TITLE OF INVENTION: Compounds and Methods for

Db 132 RPLGRFTPTMPPRVADHVAANVVFG--NPLRDIRGGPRLEPR 173

RESULT 12

US-08-997-080-112
; Sequence 112, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-080-112

Query Match 11.6%; Score 116; DB 2; Length 167;

Best Local Similarity 30.1%; Pred. No. 1.6e-05;

Matches 44; Conservative 19; Mismatches 47; Indels 36; Gaps 9;

QY 9 LESSGANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQVGGPYDAALA 67

Db 27 IPTASADPCDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVG----QSVG-----TYA 76

QY 68 TNF-----LPRGTSQANIDEGKRLFALANQCPNTPVVGYSOGAALIAAAV--- 115

Db 77 VNYPAGFDFDKSAPMGAAADAS---GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131

QY 116 -----SELGAVKEQVKGVALFG 133

Db 132 RPLGRFTPTMPPRVADHVAANVVFG 157

RESULT 13

US-08-997-362-112
; Sequence 112, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth

; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-362-112

Query Match 11.6%; Score 116; DB 2; Length 167;
Best Local Similarity 30.1%; Pred. No. 1.6e-05;
Matches 44; Conservative 19; Mismatches 47; Indels 36; Gaps 9;

QY 9 LESSGANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQVGGPYDAALA 67

Db 27 IPTASADPCDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVG----QSVG-----TYA 76

QY 68 TNF-----LPRGTSQANIDEGKRLFALANQCPNTPVVGYSOGAALIAAAV--- 115

Db 77 VNYPAGFDFDKSAPMGAAADAS---GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131

QY 116 -----SELGAVKEQVKGVALFG 133

Db 132 RPLGRFTPTMPPRVADHVAANVVFG 157

RESULT 14
US-09-095-855-112
; Sequence 112, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208

; NUMBER OF SEQ ID NOS: 194

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2003, 15:01:13 ; Search time 36 seconds
(without alignments)
718.073 Million cell updates/sec

Title: US-09-873-075a-1
Perfect score: 999
Sequence: 1 QLGAIENGLESGSANACPD.....SYTIEARGEARFLDRIR 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:	*
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6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:	*
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9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:	*
10:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:	*
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16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:	*
17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:	*
18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:	*
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:	*
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:	*
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:	*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:	*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:	*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	999	100.0	194	23	AA198435
2	996	99.7	194	21	AA13715
3	995	99.6	194	21	AA13706
4	995	99.6	194	23	AA13706
5	995	99.6	194	23	AA13706
6	995	99.6	194	23	AA13706
7	993	99.4	194	21	AA13707
8	993	99.4	194	23	AA13707
9	992	99.3	194	21	AA13703
10	991	99.2	194	21	AA13704

11	991	99.2	194	23	AA13704	Mutant Humicola in
12	991	99.2	246	17	AA13705	H. insolens lipase
13	990	99.1	194	21	AA13705	H. insolens mutant
14	990	99.1	194	21	AA13711	H. insolens mutant
15	990	99.1	194	23	AA13711	Mutant Humicola in
16	989	99.0	194	21	AA13710	H. insolens mutant
17	989	99.0	194	23	AA13710	Mutant Humicola in
18	988	98.9	194	23	AA13710	Mutant Humicola in
19	987	98.8	194	21	AA13717	H. insolens mutant
20	985	98.6	194	21	AA13716	H. insolens mutant
21	984	98.5	194	21	AA13709	Mutant Humicola in
22	984	98.5	194	23	AA13709	Mutant Humicola in
23	983	98.4	194	23	AA13709	Mutant Humicola in
24	983	98.4	194	23	AA13709	Mutant Humicola in
25	983	98.4	194	23	AA13709	Mutant Humicola in
26	982	98.3	194	21	AA13708	H. insolens mutant
27	978	97.9	194	23	AA13708	Mutant Humicola in
28	978	97.9	194	23	AA13708	Mutant Humicola in
29	977	97.8	194	21	AA13718	H. insolens mutant
30	977	97.8	194	23	AA13718	Mutant Humicola in
31	976	97.7	194	23	AA13718	Mutant Humicola in
32	976	97.7	194	23	AA13718	Mutant Humicola in
33	974	97.5	194	21	AA13719	H. insolens mutant
34	973	97.4	194	23	AA13719	Mutant Humicola in
35	971	97.2	194	21	AA13712	H. insolens mutant
36	971	97.2	194	21	AA13714	Mutant Humicola in
37	969	97.0	194	23	AA13714	Mutant Humicola in
38	965	96.6	194	21	AA13713	H. insolens mutant
39	960	96.1	194	23	AA13713	Mutant Humicola in
40	955	95.6	194	23	AA13713	Mutant Humicola in
41	955	95.6	194	23	AA13713	Mutant Humicola in
42	954	95.5	194	23	AA13713	Mutant Humicola in
43	954	95.5	194	23	AA13713	Mutant Humicola in
44	954	95.5	194	23	AA13713	Mutant Humicola in
45	953	95.4	194	23	AA13713	Mutant Humicola in

ALIGNMENTS

RESULT 1
AA198435
ID AA198435 standard; protein; 194 AA.
AC
AA198435;
XX
XX
25-JUN-2002 (first entry)
DT
XX
Wild-type Humicola insolens mature cutinase.
DE
XX
Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin.
KW
XX
Humicola insolens strain DSM 1800.
OS
XX
WO200192502-A1.
XX
XX
06-DEC-2001.
XX
XX
22-MAY-2001; 2001WO-DK00350.
PF
XX
02-JUN-2000; 2000DK-0000861.
PR
23-OCT-2000; 2000DK-0001577.
PR
24-NOV-2000; 2000DK-0001772.
PR
19-JAN-2001; 2001DK-0000100.
XX
(NOVO) NOVOZYMES AS.
XX
Svendsen A, Glad SOS, Fukuyama S, Matsui T;
WPI; 2002-216714/27.
XX
Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
oligomers of poly(ethylene terephthalate), comprises a substitution of

PT amino acid residues corresponding to positions of Humicola insolens
 XX cutinase -
 XX Disclosure; Page 36; 4lpp; English.
 XX The present sequence is the wild-type mature cutinase from Humicola
 CC insolens strain DSM 1800, which was used to generate mutant cutinases
 CC (see ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes
 CC capable of hydrolysing the substrate cutin. The mutant cutinases have
 CC improved thermostability, and are used for enzymatic hydrolysis
 CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
 CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
 XX Sequence 194 AA;
 SQ Query Match 100.0%; Score 999; DB 23; Length 194;
 Best Local Similarity 100.0%; Pred. No. 3.4e-100;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWQGVGG 60
 DB 1 QLGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWQGVGG 60
 QY 61 PYDAALATNLFPRGTSQANIDEGKRLFALANOKCPNTPVAGYSQGAALIAAAVSELGG 120
 DB 61 PYDAALATNLFPRGTSQANIDEGKRLFALANOKCPNTPVAGYSQGAALIAAAVSELGG 120
 QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194
 RESULT 2
 AAB13715
 ID AAB13715 standard; Protein; 194 AA.
 AC AAB13715;
 XX 17-NOV-2000 (first entry)
 DT H. insolens mutant cutinase, E1790 substitution.
 DE Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX Humicola insolens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 179 /note= "Wild-type Glu substituted by Gln"
 FT WO200034450-A1.
 XX 15-JUN-2000.
 PD 03-DEC-1999; 99WO-DK00678.
 XX 04-DEC-1998; 98DK-0001604.
 PR 09-DEC-1998; 98US-0111591.
 PR 09-MAR-1999; 99DK-0000330.
 PR 16-MAR-1999; 99US-0124671.
 XX (NOVO) NOVO-NORDISK AS.
 XX Abo M, Fukuyama S, Svendsen A, Matsui T;
 XX WPI; 2000-482424/42.
 DR

XX Thermostable variant of parent fungal cutinase useful for dyeing
 PT polyester yarn or fabric, comprises substitution of amino acid residues
 PT at predetermined positions from the N-terminal amino acid -
 XX Example 1; Page -; 79pp; English.
 PS Site-directed mutagenesis was carried out on wild-type Humicola insolens
 XX cutinase, to produce the present sequence. The introduced substitution
 CC improves the thermostability of the cutinase enzyme. Cutinases are
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
 CC thermostability are useful since they can withstand higher processing
 CC temperatures.
 CC Note: the present sequence is not shown in the specification but is
 CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID
 CC 2 of patent: US 5,827,719.
 XX Sequence 194 AA;
 SQ Query Match 99.7%; Score 996; DB 21; Length 194;
 Best Local Similarity 99.5%; Pred. No. 7.2e-100;
 Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWQGVGG 60
 DB 1 QLGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWQGVGG 60
 QY 61 PYDAALATNLFPRGTSQANIDEGKRLFALANOKCPNTPVAGYSQGAALIAAAVSELGG 120
 DB 61 PYDAALATNLFPRGTSQANIDEGKRLFALANOKCPNTPVAGYSQGAALIAAAVSELGG 120
 QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194
 RESULT 3
 AAB13706
 ID AAB13706 standard; Protein; 194 AA.
 AC AAB13706;
 XX 17-NOV-2000 (first entry)
 DT H. insolens mutant cutinase, E47K substitution.
 DE Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX Humicola insolens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 47 /note= "Wild-type Glu substituted by Lys"
 FT WO200034450-A1.
 XX 15-JUN-2000.
 PD 03-DEC-1999; 99WO-DK00678.
 XX 04-DEC-1998; 98DK-0001604.
 PR 09-DEC-1998; 98US-0111591.
 PR 09-MAR-1999; 99DK-0000330.

PR 16-MAR-1999; 99US-0124671.
XX (NOVO) NOVO-NORDISK AS.
PA Abo M, Fukuyama S, Svendsen A, Matsui T;
PI WPI; 2000-482424/42.
XX
XX The most stable variant of parent fungal cutinase useful for dyeing
PT polyester yarn or fabric, comprises substitution of amino acid residues
PT at predetermined positions from the N-terminal amino acid -
XX
XX Claim 15; Page -: 79pp; English.
XX
XX Site-directed mutagenesis was carried out on wild-type Humicola insolens
CC cutinase, to produce the present sequence. The introduced substitution
CC improves the thermostability of the cutinase enzyme. Cutinases are
CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
CC may be used in the enzymatic hydrolysis of cyclic oligomers of
CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
CC thermostability are useful since they can withstand higher processing
CC temperatures.
CC Note: the present sequence is not shown in the specification but is
CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID
CC 2 of patent: US 5,827,719.
XX
XX Sequence 194 AA;
SQ
Query Match 99.6%; Score 995; DB 21; Length 194;
Best Local Similarity 99.5%; Pred. No. 9.3e-100;
Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIOGVG 60
DB 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIOGVG 60
QY 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELG 120
DB 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELG 120
QY 121 AVKEQKGVALFGYTONLQNRGIPNYPRTKVFNCVGDVCTGLTIITPAHLSTYIEA 180
DB 121 AVKEQKGVALFGYTONLQNRGIPNYPRTKVFNCVGDVCTGLTIITPAHLSTYIEA 180
QY 181 RGEAARFLDRIRA 194
DB 181 RGEAARFLDRIRA 194
RESULT 4
ABB76837
XX ID ABB76837 standard; Protein; 194 AA.
XX AC ABB76837;
XX
XX 25-JUN-2002 (first entry)
XX
XX Mutant Humicola insolens mature cutinase #11.
XX
XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
XX
XX Humicola insolens strain DSM 1800.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 164
FT /note= "Wild-type Thr substituted by Ser"
XX
XX WO200192502-A1.
XX
XX 06-DEC-2001.
XX

PF 22-MAY-2001; 2001WO-DK00350.
XX
XX 02-JUN-2000; 2000DK-0000861.
PR 23-OCT-2000; 2000DK-0001577.
PR 24-NOV-2000; 2000DK-0001772.
PR 19-JAN-2001; 2001DK-0000100.
XX
XX (NOVO) NOVOZYMES AS.
PA
XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;
PI WPI; 2002-216714/27.
XX
XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
PT oligomers of poly(ethylene terephthalate), comprises a substitution of
PT amino acid residues corresponding to positions of Humicola insolens
PT cutinase -
XX
XX Claim 8; Page -: 41pp; English.
XX
XX The present invention relates to wild-type mature cutinase from Humicola
CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
CC have improved thermostability, and are used for enzymatic hydrolysis
CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
CC Note: the present sequence is not shown in the specification, but is
CC derived from the wild-type cutinase sequence shown on page 36.
XX
XX Sequence 194 AA;
SQ
Query Match 99.6%; Score 995; DB 23; Length 194;
Best Local Similarity 99.5%; Pred. No. 9.3e-100;
Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIOGVG 60
DB 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIOGVG 60
QY 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELG 120
DB 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELG 120
QY 121 AVKEQKGVALFGYTONLQNRGIPNYPRTKVFNCVGDVCTGLTIITPAHLSTYIEA 180
DB 121 AVKEQKGVALFGYTONLQNRGIPNYPRTKVFNCVGDVCTGLTIITPAHLSTYIEA 180
QY 181 RGEAARFLDRIRA 194
DB 181 RGEAARFLDRIRA 194
RESULT 5
ABB76838
XX ID ABB76838 standard; Protein; 194 AA.
XX AC ABB76838;
XX
XX 25-JUN-2002 (first entry)
XX
XX Mutant Humicola insolens mature cutinase #12.
XX
XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
XX
XX Humicola insolens strain DSM 1800.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 174
FT /note= "Wild-type Leu substituted by Phe"
XX
XX WO200192502-A1.

```
XX PD 06-DEC-2001.
XX PF 22-MAY-2001; 2001WO-DK00350.
XX PR 02-JUN-2000; 2000DK-0000861.
XX PR 23-OCT-2000; 2000DK-0001577.
XX PR 24-NOV-2000; 2000DK-0001772.
XX PR 19-JAN-2001; 2001DK-0000100.
XX PA (NOVO ) NOVOZYMES AS.
XX PI Svendsen A, Glad SOS, Fukuyama S, Matsui T;
XX DR WPI; 2002-216714/27.
XX PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
XX PT oligomers of poly(ethylene terephthalate), comprises a substitution of
XX PT amino acid residues corresponding to positions of Humicola insolens
XX PS cutinase -
XX PS Claim 8; Page -: 41pp; English.
XX CC The present invention relates to wild-type mature cutinase from Humicola
XX CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
XX CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
XX CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
XX CC have improved thermostability, and are used for enzymatic hydrolysis
XX CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
XX CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
XX CC Note: the present sequence in not shown in the specification, but is
XX CC derived from the wild-type cutinase sequence shown on page 36.
XX SQ Sequence 194 AA;

Query Match 99.6%; Score 995; DB 23; Length 194;
Best Local Similarity 99.5%; Pred. No. 9.3e-100;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLGAIENGLESGSNACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGG 60
Db 1 QLGAIENGLESGSNACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGG 60

Qy 61 PYDAALATNFTLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
Db 61 PYDAALATNFTLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120

Qy 121 AVKEQVKGVALLFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGTLTIITPAHLSYITIEA 180
Db 121 AVKEQVKGVALLFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGTLTIITPAHLSYITIEA 180

Qy 181 RGEAARFLDRIRA 194
Db 181 RGEAARFLDRIRA 194

RESULT 6
ABB76844
ID ABB76844 standard; Protein; 194 AA.
XX AC ABB76844;
XX AC ABB76844;
XX DT 25-JUN-2002 (first entry)
XX DE Mutant Humicola insolens mature cutinase #18.
XX KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
XX OS Humicola insolens strain DSM 1800.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 130
```

```
FT XX /note= "Wild-type Arg substituted by Val"
PN XX WO200192502-A1.
XX PD 06-DEC-2001.
XX PF 22-MAY-2001; 2001WO-DK00350.
XX PR 02-JUN-2000; 2000DK-0000861.
XX PR 23-OCT-2000; 2000DK-0001577.
XX PR 24-NOV-2000; 2000DK-0001772.
XX PR 19-JAN-2001; 2001DK-0000100.
XX PA (NOVO ) NOVOZYMES AS.
XX PI Svendsen A, Glad SOS, Fukuyama S, Matsui T;
XX DR WPI; 2002-216714/27.
XX PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
XX PT oligomers of poly(ethylene terephthalate), comprises a substitution of
XX PT amino acid residues corresponding to positions of Humicola insolens
XX PS cutinase -
XX PS Claim 8; Page -: 41pp; English.
XX CC The present invention relates to wild-type mature cutinase from Humicola
XX CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
XX CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
XX CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
XX CC have improved thermostability, and are used for enzymatic hydrolysis
XX CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
XX CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
XX CC Note: the present sequence in not shown in the specification, but is
XX CC derived from the wild-type cutinase sequence shown on page 36.
XX SQ Sequence 194 AA;

Query Match 99.6%; Score 995; DB 23; Length 194;
Best Local Similarity 99.5%; Pred. No. 9.3e-100;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLGAIENGLESGSNACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGG 60
Db 1 QLGAIENGLESGSNACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGG 60

Qy 61 PYDAALATNFTLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
Db 61 PYDAALATNFTLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120

Qy 121 AVKEQVKGVALLFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGTLTIITPAHLSYITIEA 180
Db 121 AVKEQVKGVALLFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGTLTIITPAHLSYITIEA 180

Qy 181 RGEAARFLDRIRA 194
Db 181 RGEAARFLDRIRA 194

RESULT 7
AAB13707
ID AAB13707 standard; Protein; 194 AA.
XX AC AAB13707;
XX AC AAB13707;
XX DT 17-NOV-2000 (first entry)
XX DE H. insolens mutant cutinase, E179X substitution.
XX KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
XX KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
XX KW protein co-ordinate.
```

OS Humicola insolens.
 XX Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 179 /note= "Wild-type Glu substituted by Asn or Gln"
 XX
 XX WO200034450-A1.
 XX
 XX 15-JUN-2000.
 XX
 XX 03-DEC-1999; 99WO-DK00678.
 XX
 XX 04-DEC-1998; 98DK-0001604.
 PR 09-DEC-1998; 98US-0111591.
 PR 09-MAR-1999; 99DK-0000330.
 PR 16-MAR-1999; 99US-0124671.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 XX
 XX Abo M., Fukuyama S., Svendsen A., Matsui T;
 XX
 XX WPI; 2000-482424/42.
 XX
 XX Thermostable variant of parent fungal cutinase useful for dyeing
 PT polyester yarn or fabric, comprises substitution of amino acid residues
 PT at predetermined positions from the N-terminal amino acid
 XX
 XX Claim 16; Page -: 79pp; English.
 XX
 XX Site-directed mutagenesis was carried out on wild-type Humicola insolens
 CC cutinase, to produce the present sequence. The introduced substitution
 CC improves the thermostability of the cutinase enzyme. Cutinases are
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
 CC thermostability are useful since they can withstand higher processing
 CC temperatures.
 CC Note: the present sequence is not shown in the specification but is
 CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID
 CC 2 of patent: US 5,827,719.
 XX
 XX Sequence 194-AA;
 SQ
 Query Match 99.4%; Score 993; DB 21; Length 194;
 Best Local Similarity 99.5%; Pred. No. 1.5e-99;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNIWIOGVG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNIWIOGVG 60
 QY 61 PYDAALATNPLRGTSQANIDEKRLFALANQKCPNTPPVAGYSOGAALIAAAVSELG 120
 DB 61 PYDAALATNPLRGTSQANIDEKRLFALANQKCPNTPPVAGYSOGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSVTIEA 180
 DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSVTIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194
 RESULT 8
 ABB76839
 ID ABB76839 standard; Protein; 194 AA.
 XX
 AC ABB76839;
 XX
 XX 25-JUN-2002 (first entry)

XX Mutant Humicola insolens mature cutinase #13.
 DE
 XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
 KW
 XX Humicola insolens strain DSM 1800.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 49 /note= "Wild-type His substituted by Tyr"
 FT
 XX WO200192502-A1.
 XX
 XX 06-DEC-2001.
 PD
 XX 22-MAY-2001; 2001WO-DK00350.
 PF
 XX 02-JUN-2000; 2000DK-0000861.
 PR 23-OCT-2000; 2000DK-0001577.
 PR 24-NOV-2000; 2000DK-0001772.
 PR 19-JAN-2001; 2001DK-0000100.
 XX
 XX (NOVO) NOVOZYMES AS.
 PA
 XX Svendsen A., Glad SOS, Fukuyama S., Matsui T;
 PI
 XX WPI; 2002-216714/27.
 DR
 XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
 PT oligomers of poly(ethylene terephthalate), comprises a substitution of
 PT amino acid residues corresponding to positions of Humicola insolens
 PT cutinase -
 XX
 XX Claim 8; Page -: 41pp; English.
 PS
 XX The present invention relates to wild-type mature cutinase from Humicola
 CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
 CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
 CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
 CC have improved thermostability, and are used for enzymatic hydrolysis
 CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
 CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
 CC Note: the present sequence in not shown in the specification, but is
 CC derived from the wild-type cutinase sequence shown on page 36.
 CC
 XX Sequence 194 AA;
 SQ
 Query Match 99.4%; Score 993; DB 23; Length 194;
 Best Local Similarity 99.5%; Pred. No. 1.5e-99;
 Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNIWIOGVG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNIWIOGVG 60
 QY 61 PYDAALATNPLRGTSQANIDEKRLFALANQKCPNTPPVAGYSOGAALIAAAVSELG 120
 DB 61 PYDAALATNPLRGTSQANIDEKRLFALANQKCPNTPPVAGYSOGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSVTIEA 180
 DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSVTIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194
 RESULT 9
 AAB13703
 ID AAB13703 standard; Protein; 194 AA.
 XX

[illegible]

Db	181	RGEARFLDRIRA	194
	RESULT 10		
	AAB13704		
ID	AAB13704	standard; Protein; 194 AA.	
XX	AC	AAB13704;	
XX	17-NOV-2000	(first entry)	
XX			
XX	H. insolens	mutant cutinase, E6X/L138I substitution.	
DE			
XX	Site directed	mutagenesis; cutinase; mutant; mutein; substitution;	
KW	thermostability;	enzyme; lipolytic; fabric finishing; yarn;	
KW	protein co-ordinate.		
XX			
OS	Humicola insolens.		
OS	Synthetic.		
XX			
Key	Location/Qualifiers		
FT	Misc-difference 6		
FT	/note= "Wild-type Glu substituted by Asn or Glu"		
FT	Misc-difference 138		
FT	/note= "Wild-type Leu substituted by Ile"		
XX			
PN	WO200034450-A1.		
XX			
PD	15-JUN-2000.		
XX			
PF	03-DEC-1999;	99WO-DK00678.	
XX			
XX	04-DEC-1998;	98DK-0001604.	
PR	09-DEC-1998;	98US-0111591.	
PR	09-MAR-1999;	99DK-0000330.	
PR	16-MAR-1999;	99US-0124671.	
XX			
PA	(NOVO)	NOVO-NORDISK AS.	
XX			
PI	Abo M, Fukuyama S, Svendsen A, Matsui T;		
PI	WPI; 2000-482424/42.		
XX			
PT	Thermostable variant of parent fungal cutinase useful for dyeing		
PT	polyester yarn or fabric, comprises substitution of amino acid residues		
PT	at predetermined positions from the N-terminal amino acid		
XX			
PS	Claim 16; Page -; 79pp; English.		
XX			
CC	Site-directed mutagenesis was carried out on wild-type Humicola insolens		
CC	cutinase, to produce the present sequence. The introduced substitution		
CC	improves the thermostability of the cutinase enzyme. Cutinases are		
CC	lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase		
CC	may be used in the enzymatic hydrolysis of cyclic oligomers of		
CC	poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from		
CC	poly(ethylene terephthalate) fibers. Cutinase variants with improved		
CC	thermostability are useful since they can withstand higher processing		
CC	temperatures.		
CC	Note: the present sequence is not shown in the specification but is		
CC	derived from the H. insolens wild-type cutinase sequence given in SEQ ID		
CC	2 of patent: US 5,827,719.		
XX			
SQ	Sequence	194 AA;	

Db 61 PYDAALATNPLPGTSQANIDEGKRLFALANQKCPNTPPVAGGYSQGAALIAAAVSELG 120
 QY 121 AVKEQKGVALFGYTONLQNRGGIPNYPRETKVFCNVGDAVCTGTLITPAHLSYTIEA 180
 Db 121 AVKEQKGVALFGYTONLQNRGGIPNYPRETKVFCNVGDAVCTGTLITPAHLSYTIEA 180
 QY 181 RGEAARFLDRIRA 194
 Db 181 RGEAARFLDRIRA 194
 RESULT 11
 ABB76845
 ID ABB76845 standard; Protein; 194 AA.
 XX
 AC ABB76845;
 XX
 DT 25-JUN-2002 (first entry)
 XX
 DE Mutant Humicola insolens mature cutinase #19.
 XX
 KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
 XX
 OS Humicola insolens strain DSM 1800.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Wild-type Gln substituted by Cys"
 FT Misc-difference 2 /note= "Wild-type Leu substituted by Val"
 FT
 XX
 PN WO200192502-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 22-MAY-2001; 2001WO-DK00350.
 XX
 PR 02-JUN-2000; 2000DK-0000861.
 PR 23-OCT-2000; 2000DK-0001577.
 PR 24-NOV-2000; 2000DK-0001772.
 PR 19-JAN-2001; 2001DK-0000100.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Glad SOS, Fukuyama S, Matsui T;
 XX
 DR WPI; 2002-216714/27.
 XX
 PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
 PT oligomers of poly(ethylene terephthalate), comprises a substitution of
 PT amino acid residues corresponding to positions of Humicola insolens
 PT cutinase -
 XX
 PS Claim 8; Page -; 41pp; English.
 PS
 CC The present invention relates to wild-type mature cutinase from Humicola
 CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
 CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
 CC enzymes capable of hydrolyzing the substrate cutin. The mutant cutinases
 CC have improved thermostability, and are used for enzymatic hydrolysis
 CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
 CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
 CC Note: the present sequence in not shown in the specification, but is
 CC derived from the wild-type cutinase sequence shown on page 36.
 CC
 XX
 SQ Sequence 194 AA;
 Query Match 99.2%; Score 991; DB 23; Length 194;
 Best Local Similarity 99.5%; Pred. No. 2.5e-99;
 Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QLCAGIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGG 60
 :|||||
 Db 2 VQAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGGP 61
 :|||||
 QY 62 YDAALATNPLPGTSQANIDEGKRLFALANQKCPNTPPVAGGYSQGAALIAAAVSELG 121
 :|||||
 Db 62 YDAALATNPLPGTSQANIDEGKRLFALANQKCPNTPPVAGGYSQGAALIAAAVSELG 121
 :|||||
 QY 122 VKEQKGVALFGYTONLQNRGGIPNYPRETKVFCNVGDAVCTGTLITPAHLSYTIEAR 181
 :|||||
 Db 122 VKEQKGVALFGYTONLQNRGGIPNYPRETKVFCNVGDAVCTGTLITPAHLSYTIEAR 181
 :|||||
 QY 182 GEAARFLDRIRA 194
 :|||||
 Db 182 GEAARFLDRIRA 194
 :|||||
 RESULT 12
 AAR95051
 ID AAR95051 standard; Protein; 246 AA.
 XX
 AC AAR95051;
 XX
 DT 17-DEC-1996 (first entry)
 XX
 DE H. insolens lipase.
 XX
 KW lipase; detergent; dishwashing; laundry; short-chain lipid.
 XX
 OS Humicola insolens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..35
 FT /label= signal_peptide
 FT Protein 36..246
 FT /label= mature_protein
 XX
 PN WO9613580-A1.
 XX
 PD 09-MAY-1996.
 XX
 PF 26-OCT-1995; 95WO-DK00427.
 XX
 PR 26-OCT-1994; 94DK-0001240.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Kauppinen S, Kofod LV, Sandal T;
 XX
 DR WPI; 1996-239493/24.
 DR N-PSDB; AAR29401.
 XX
 PT Isolated DNA encoding lipolytic enzyme - derived from Humicola
 PT insolens DSM1800, used partic. as detergent additive for laundry and
 PT dishwashing compsns.
 XX
 PS Disclosure; Page 52; 63pp; English.
 PS
 CC The present sequence is that of an enzyme with lipolytic activity,
 CC derived from Humicola insolens DSM1800. The enzyme has a mol. wt. of
 CC about 20-21 kDa, a pI in the range of 709, a pH optimum of about 8 and
 CC has specificity towards short-chain lipid substrates. It can be used as
 CC a detergent additive, partic. in compsns. for laundry washing or
 CC dishwashing.
 CC
 XX
 SQ Sequence 246 AA;
 Query Match 99.2%; Score 991; DB 17; Length 246;
 Best Local Similarity 99.5%; Pred. No. 3.5e-99;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLCAGIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGG 60
 :|||||

QY 2 LGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGGP 61
 :|||||
 Db 2 VQAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGGP 61
 :|||||
 QY 62 YDAALATNPLPGTSQANIDEGKRLFALANQKCPNTPPVAGGYSQGAALIAAAVSELG 121
 :|||||
 Db 62 YDAALATNPLPGTSQANIDEGKRLFALANQKCPNTPPVAGGYSQGAALIAAAVSELG 121
 :|||||
 QY 122 VKEQKGVALFGYTONLQNRGGIPNYPRETKVFCNVGDAVCTGTLITPAHLSYTIEAR 181
 :|||||
 Db 122 VKEQKGVALFGYTONLQNRGGIPNYPRETKVFCNVGDAVCTGTLITPAHLSYTIEAR 181
 :|||||
 QY 182 GEAARFLDRIRA 194
 :|||||
 Db 182 GEAARFLDRIRA 194
 :|||||
 RESULT 12
 AAR95051
 ID AAR95051 standard; Protein; 246 AA.
 XX
 AC AAR95051;
 XX
 DT 17-DEC-1996 (first entry)
 XX
 DE H. insolens lipase.
 XX
 KW lipase; detergent; dishwashing; laundry; short-chain lipid.
 XX
 OS Humicola insolens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..35
 FT /label= signal_peptide
 FT Protein 36..246
 FT /label= mature_protein
 XX
 PN WO9613580-A1.
 XX
 PD 09-MAY-1996.
 XX
 PF 26-OCT-1995; 95WO-DK00427.
 XX
 PR 26-OCT-1994; 94DK-0001240.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Kauppinen S, Kofod LV, Sandal T;
 XX
 DR WPI; 1996-239493/24.
 DR N-PSDB; AAR29401.
 XX
 PT Isolated DNA encoding lipolytic enzyme - derived from Humicola
 PT insolens DSM1800, used partic. as detergent additive for laundry and
 PT dishwashing compsns.
 XX
 PS Disclosure; Page 52; 63pp; English.
 PS
 CC The present sequence is that of an enzyme with lipolytic activity,
 CC derived from Humicola insolens DSM1800. The enzyme has a mol. wt. of
 CC about 20-21 kDa, a pI in the range of 709, a pH optimum of about 8 and
 CC has specificity towards short-chain lipid substrates. It can be used as
 CC a detergent additive, partic. in compsns. for laundry washing or
 CC dishwashing.
 CC
 XX
 SQ Sequence 246 AA;
 Query Match 99.2%; Score 991; DB 17; Length 246;
 Best Local Similarity 99.5%; Pred. No. 3.5e-99;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLCAGIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGG 60
 :|||||

Db 36 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIOGVGG 95
QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAGGYSGAALIAAAVSELSS 120
Db 96 PYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAGGYSGAALIAAAVSELSS 155
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVKFCNVGDVCTGTLTIITPAHLSYTTIEA 180
Db 156 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVKFCNVGDVCTGTLTIITPAHLSYTTIEA 215
QY 181 RGEAARFLDRIRA 194
Db 216 RGEAARFLDRIRA 229
RESULT 13
AABI3705
ID AABI3705 standard; Protein; 194 AA.
XX
AC AABI3705;
XX
DT 17-NOV-2000 (first entry)
XX
DE H. insolens mutant cutinase, A14P/E47K substitution.
XX
KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
KW protein co-ordinate.
XX
OS Humicola insolens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 14
FT /note= "Wild-type Ala substituted by Pro"
FT
FT Misc-difference 47
FT /note= "Wild-type Glu substituted by Lys"
XX
PN WO200034450-A1.
XX
PD 15-JUN-2000.
XX
XX 03-DEC-1999; 99WO-DK00678.
XX
XX 04-DEC-1998; 98DK-0001604.
PR 09-DEC-1998; 98US-0111591.
PR 09-MAR-1999; 99DK-0000330.
PR 16-MAR-1999; 99US-0124671.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
XX Abo M, Fukuyama S, Svendsen A, Matsui T;
XX WPI; 2000-482424/42.
XX
XX Thermostable variant of parent fungal cutinase useful for dyeing
PT polyester yarn or fabric, comprises substitution of amino acid residues
PT at predetermined positions from the N-terminal amino acid
XX
XX Claim 16; Page -: 79pp; English.
XX
XX Site-directed mutagenesis was carried out on wild-type Humicola insolens
CC cutinase, to produce the present sequence. The introduced substitution
CC improves the thermostability of the cutinase enzyme. Cutinases are
CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
CC may be used in the enzymatic hydrolysis of cyclic oligomers of
CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
CC thermostability are useful since they can withstand higher processing
CC temperatures.
CC Note: the present sequence is not shown in the specification but is
CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID
CC 2 of patent: US 5,827,719.

XX Sequence 194 AA;
SQ
Query Match 99.1%; Score 990; DB 21; Length 194;
Best Local Similarity 99.0%; Pred. No. 3.2e-99;
Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIOGVGG 60
Db 1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIOGVGG 60
QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAGGYSGAALIAAAVSELSS 120
Db 61 PYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAGGYSGAALIAAAVSELSS 120
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVKFCNVGDVCTGTLTIITPAHLSYTTIEA 180
Db 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVKFCNVGDVCTGTLTIITPAHLSYTTIEA 180
QY 181 RGEAARFLDRIRA 194
Db 181 RGEAARFLDRIRA 194
RESULT 14
AABI3711
ID AABI3711 standard; Protein; 194 AA.
XX
AC AABI3711;
XX
DT 17-NOV-2000 (first entry)
XX
DE H. insolens mutant cutinase, E47K/D63N substitution.
XX
KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
KW protein co-ordinate.
XX
OS Humicola insolens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 47
FT /note= "Wild-type Glu substituted by Lys"
FT
FT Misc-difference 63
FT /note= "Wild-type Asp substituted by Asn"
XX
PN WO200034450-A1.
XX
PD 15-JUN-2000.
XX
XX 03-DEC-1999; 99WO-DK00678.
XX
XX 04-DEC-1998; 98DK-0001604.
PR 09-DEC-1998; 98US-0111591.
PR 09-MAR-1999; 99DK-0000330.
PR 16-MAR-1999; 99US-0124671.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
XX Abo M, Fukuyama S, Svendsen A, Matsui T;
XX WPI; 2000-482424/42.
XX
XX Thermostable variant of parent fungal cutinase useful for dyeing
PT polyester yarn or fabric, comprises substitution of amino acid residues
PT at predetermined positions from the N-terminal amino acid
XX
XX Claim 16; Page -: 79pp; English.
XX
XX Site-directed mutagenesis was carried out on wild-type Humicola insolens
CC cutinase, to produce the present sequence. The introduced substitution
CC improves the thermostability of the cutinase enzyme. Cutinases are

CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
CC may be used in the enzymatic hydrolysis of cyclic oligomers of
CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
CC thermostability are useful since they can withstand higher processing
CC temperatures.
CC Note: the present sequence is not shown in the specification but is
CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID
CC 2 of patent: US 5,827,719.

XX Sequence 194 AA;

Query Match 99.1%; Score 990; DB 21; Length 194;
Best Local Similarity 99.0%; Pred. No. 3.2e-99;
Matches 192; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEPGNMGITVGPALANGLESIRNIWIOGVGG 60
DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEPGNMGITVGPALANGLESIRNIWIOGVGG 60
QY 61 PYDAALATNLFPRGTQANIDEKRLFALANOKCPNTPVVAGGYSOGAALIAAAVSELG 120
DB 61 PYDAALATNLFPRGTQANIDEKRLFALANOKCPNTPVVAGGYSOGAALIAAAVSELG 120
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRETRKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRETRKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
QY 181 RGEAARFLDRIRARA 194
DB 181 RGEAARFLDRIRARA 194

RESULT 15

ABB76829
ID ABB76829 standard; Protein; 194 AA.
XX ABB76829;
XX AC ABB76829;
XX 25-JUN-2002 (first entry)
XX Mutant Humicola insolens mature cutinase #3.
DE Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
XX Humicola insolens strain DSM 1800.
OS Synthetic.

XX Key Location/Qualifiers
FT Misc-difference 44
FT /note= "Wild-type Asn substituted by Asp"
FT Misc-difference 130
FT /note= "Wild-type Ala substituted by Val"

XX WO200192502-A1.
XX 06-DEC-2001.
XX 22-MAY-2001; 2001WO-DK00350.
XX 02-JUN-2000; 2000DK-0000861.
XX 23-OCT-2000; 2000DK-0001577.
XX 24-NOV-2000; 2000DK-0001772.
XX 19-JAN-2001; 2001DK-0000100.
XX (NOVO) NOVOZYMES AS.
XX Svendsen A, Glad SO5, Fukuyama S, Matsui T;
XX WPI; 2002-216714/27.

XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
PT oligomers of poly(ethylene terephthalate), comprises a substitution of

PT. amino acid residues corresponding to positions of Humicola insolens
cutinase -
XX
XX Claim 8; Page -; 4lpp; English.
XX
XX The present invention relates to wild-type mature cutinase from Humicola
insolens strain DSM 1800 (AAM48435), which was used to generate mutant
cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
have improved thermostability, and are used for enzymatic hydrolysis
of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
Note: the present sequence is not shown in the specification, but is
derived from the wild-type cutinase sequence shown on page 36.

XX Sequence 194 AA;

Query Match 99.1%; Score 990; DB 23; Length 194;
Best Local Similarity 99.0%; Pred. No. 3.2e-99;
Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEPGNMGITVGPALANGLESIRNIWIOGVGG 60
DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEPGNMGITVGPALANGLESIRNIWIOGVGG 60
QY 61 PYDAALATNLFPRGTQANIDEKRLFALANOKCPNTPVVAGGYSOGAALIAAAVSELG 120
DB 61 PYDAALATNLFPRGTQANIDEKRLFALANOKCPNTPVVAGGYSOGAALIAAAVSELG 120
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRETRKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRETRKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
QY 181 RGEAARFLDRIRARA 194
DB 181 RGEAARFLDRIRARA 194

Search completed: January 2, 2003, 15:05:20
Job time : 37 secs

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OM protein - protein search, using sw model

Run on: January 2, 2003, 15:06:24 ; Search time 10 Seconds
(without alignments)
367.659 Million cell updates/sec

Title: US-09-873-075A-1

Perfect score: 999

Sequence: 1 QLGAIENGLESANACPDPA.....SYTIEARGEARFLDRIRA 194

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Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	999	100.0	194	10	US-09-873-075A-1	Sequence 1, Appli
2	268	26.8	255	9	US-10-114-116-1	Sequence 1, Appli
3	268	26.8	255	9	US-10-114-115A-1	Sequence 1, Appli
4	197.5	19.8	217	10	US-09-791-171-10	Sequence 10, Appl
5	187.5	18.8	219	10	US-09-791-171-14	Sequence 14, Appl
6	179	17.9	226	10	US-09-791-171-52	Sequence 52, Appl
7	167.5	16.8	262	10	US-09-791-171-56	Sequence 56, Appl
8	145	14.5	285	9	US-10-051-643-197	Sequence 197, App
9	119	11.9	748	9	US-10-051-643-154	Sequence 154, App
10	116	11.6	167	9	US-10-051-643-112	Sequence 112, App
11	86.5	8.7	200	10	US-09-950-368-18	Sequence 18, Appl
12	83	8.3	1356	9	US-10-077-111-10	Sequence 10, Appl
13	82.5	8.3	398	10	US-09-815-242-11920	Sequence 11920, A
14	76.5	7.7	309	9	US-09-738-626-6668	Sequence 6668, Ap
15	76.5	7.7	1008	12	US-10-017-828-7	Sequence 7, Appli
16	76.5	7.7	1008	12	US-10-017-828-8	Sequence 8, Appli
17	76	7.6	424	10	US-09-815-242-13704	Sequence 13704, A
18	74	7.4	1293	10	US-09-815-242-10079	Sequence 10079, A
19	73	7.3	1454	10	US-09-854-799-22	Sequence 22, Appl

20	73	7.3	1454	10	US-09-854-799-26	Sequence 26, Appl
21	72	7.2	341	9	US-09-738-626-6080	Sequence 6080, Ap
22	72	7.2	424	10	US-09-815-242-10252	Sequence 10252, A
23	72	7.2	778	10	US-09-841-132-193	Sequence 193, App
24	72	7.2	978	12	US-10-007-693-65	Sequence 65, Appl
25	72	7.2	1530	10	US-09-841-132-178	Sequence 178, App
26	71.5	7.2	582	10	US-09-815-242-13898	Sequence 13898, A
27	71	7.1	1531	12	US-10-007-693-98	Sequence 98, Appl
28	70.5	7.1	144	10	US-09-923-299-810	Sequence 810, App
29	70	7.0	617	10	US-09-815-242-13228	Sequence 13228, A
30	70	7.0	1344	9	US-09-738-626-6888	Sequence 6888, Ap
31	70	7.0	1616	9	US-09-712-363-262	Sequence 262, App
32	69.5	7.0	399	9	US-09-738-626-4632	Sequence 4632, Ap
33	69.5	7.0	572	10	US-09-815-242-10049	Sequence 10049, A
34	69	6.9	261	10	US-09-940-037A-29	Sequence 29, Appl
35	69	6.9	334	9	US-09-738-626-3582	Sequence 3582, Ap
36	69	6.9	406	10	US-09-815-242-12004	Sequence 12004, A
37	69	6.9	426	9	US-10-124-800-10	Sequence 10, Appl
38	69	6.9	611	10	US-09-748-107-4	Sequence 4, Appl1
39	69	6.9	694	9	US-09-738-626-3867	Sequence 3867, Ap
40	69	6.9	1454	10	US-09-854-799-32	Sequence 32, Appl
41	69	6.9	2910	9	US-10-124-800-2	Sequence 2, Appl1
42	68	6.8	315	10	US-09-764-853-793	Sequence 793, App
43	68	6.8	1510	9	US-09-738-626-3707	Sequence 3707, Ap
44	67.5	6.8	460	9	US-09-813-453A-39	Sequence 39, Appl
45	67.5	6.8	516	9	US-09-738-626-6665	Sequence 6665, Ap

ALIGNMENTS

RESULT 1
US-09-873-075A-1
; Sequence 1, Application US/09873075A
; Patent No. US20020123123A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Schroder Glad, Sanne
; APPLICANT: Fukuyama, Shiro
; APPLICANT: Matsui, Tomoko
; TITLE OF INVENTION: Cutinase variants
; FILE REFERENCE: 10038.200-US
; CURRENT APPLICATION NUMBER: US/09/873,075A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 194
; ORGANISM: Humicola insolens
US-09-873-075A-1

Query Match 100.0%; Score 999; DB 10; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESHIRNIWIGVGC	60
Db	1	QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESHIRNIWIGVGC	60
QY	61	PYDAALATNFLPRGTSGQANIDEGKRLFALANOKCPTPVVAGGYSGAALIAAAVSELG	120
Db	61	PYDAALATNFLPRGTSGQANIDEGKRLFALANOKCPTPVVAGGYSGAALIAAAVSELG	120
QY	121	AVKEQVGVALLFGYTONLQNRGIPNYPRETRKVCNVDGAVCTGTLITPAHLSYITIA	180
Db	121	AVKEQVGVALLFGYTONLQNRGIPNYPRETRKVCNVDGAVCTGTLITPAHLSYITIA	180
QY	181	RGEARFLDRIRA 194	
Db	181	RGEARFLDRIRA 194	

Db 188 ASKISSVLLFG---DPYKGRALPNVDASRVHTVCHAGDTICENSIVILPAHLTYADVAVS 244
 QY 183 EA 184
 Db 245 AA 246
 RESULT 4
 US-09-791-171-10
 ; Sequence 10, Application US/09791171
 ; Patent No. US20020094336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDERSEN, Peter
 ; APPLICANT: NIELSEN, Rikke
 ; APPLICANT: OETTINGER, Thomas
 ; APPLICANT: RASMUSSEN, Peter Birk
 ; APPLICANT: ROSENKRANDS, Ida
 ; APPLICANT: WELDLING, Karin
 ; APPLICANT: FLORIO, Walter
 ; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
 ; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
 ; FILE REFERENCE: 670001-2002.1
 ; CURRENT APPLICATION NUMBER: US/09/791,171
 ; CURRENT FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 09/050,739
 ; PRIOR FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 0376/97
 ; PRIOR FILING DATE: 1997-04-02
 ; PRIOR APPLICATION NUMBER: 1277/97
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/044,624
 ; PRIOR FILING DATE: 1997-04-18
 ; PRIOR APPLICATION NUMBER: 60/070,488
 ; PRIOR FILING DATE: 1998-01-05
 ; NUMBER OF SEQ ID NOS: 173
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 217
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium tuberculosis
 US-09-791-171-10.
 Query Match 19.8%; Score 197.5; DB 10; Length 217;
 Best Local Similarity 30.8%; Pred. No. 1.1e-12;
 Matches 61; Conservative 26; Mismatches 88; Indels 23; Gaps
 QY 8 GLESGANACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGGPYDAALA 67
 Db 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGGRSIGVYA 76
 QY 68 TNFLP-----RGTQANIDEGKRLFALANQKCPNTVPVAGGYSGAALIAAAVSELSGAVK 123
 Db 77 VNYPASDDYRASASNGSDSAHIQRTVASCPTNTRIVGGYSQGAATVIDLSTAMPAPA 136
 QY 124 EQKGVGALF-----GYTONLQNRGGIPNYP---RERTKVFNCVNGDAVCTGLTIITPAHLS 175
 Db 137 DHVAVALFGEPPSSGFSMLWGGSLPTIGPLYSKKTINLCAPDDPCTGCGNIM-AHVS 195
 QY 176 YTIEA-RGEAARFLDRDI 192
 Db 196 YVQSGMTSQAATFAANRL 213
 RESULT 5
 US-09-791-171-14
 ; Sequence 14, Application US/09791171
 ; Patent No. US20020094336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDERSEN, Peter
 ; APPLICANT: NIELSEN, Rikke
 ; APPLICANT: OETTINGER, Thomas
 ; APPLICANT: RASMUSSEN, Peter Birk
 ; APPLICANT: ROSENKRANDS, Ida
 US-10-114-115A-1
 ; Sequence 1, Application US/10114115A
 ; Patent No. US20020173013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sumitomo Chemical Co. Ltd.
 ; TITLE OF INVENTION: Esterase Genes and Use thereof
 ; FILE REFERENCE: P150409
 ; CURRENT APPLICATION NUMBER: US/10/114,115A
 ; CURRENT FILING DATE: 2002-04-03
 ; PRIOR APPLICATION NUMBER: 09/585,468
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 5
 ; SEQ ID NO 1
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Aspergillus flavus
 US-10-114-115A-1
 Query Match 26.8%; Score 268; DB 9; Length 255;
 Best Local Similarity 34.6%; Pred. No. 1.1e-19;
 Matches 63; Conservative 30; Mismatches 69; Indels 20; Gaps
 QY 11 SGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHI--RNIIWQVGGPYDAALAT 68
 Db 77 NGFTGACTDVTYLFARGTSEPGNVLVGPPLAEAFEGAVGASALSFQGVNG-YASAV-E 134
 QY 69 NFLPRGTQANIDEGKRLFALANQ-----KCPNTPVWAGGYSGAALIAAAVSELSGAV 122
 Db 135 GYLGG-----EAAGSKAMASQASDILSKCPDTKLVMSGYSGQCGIIVHNAVEQLPAEH 187
 QY 123 KEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSYTIETARG 182
 Db 188 ASKISSVLLFG---DPYKGRALPNVDASRVHTVCHAGDTICENSIVILPAHLTYADVAVS 244
 QY 183 EA 184
 Db 245 AA 246
 RESULT 3
 US-10-114-115A-1
 ; Sequence 1, Application US/10114115A
 ; Patent No. US20020173013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sumitomo Chemical Co. Ltd.
 ; TITLE OF INVENTION: Esterase Genes and Use thereof
 ; FILE REFERENCE: P150409
 ; CURRENT APPLICATION NUMBER: US/10/114,115A
 ; CURRENT FILING DATE: 2002-04-03
 ; PRIOR APPLICATION NUMBER: 09/585,468
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 5
 ; SEQ ID NO 1
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Aspergillus flavus
 US-10-114-115A-1
 Query Match 26.8%; Score 268; DB 9; Length 255;
 Best Local Similarity 34.6%; Pred. No. 1.1e-19;
 Matches 63; Conservative 30; Mismatches 69; Indels 20; Gaps
 QY 11 SGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHI--RNIIWQVGGPYDAALAT 68
 Db 77 NGFTGACTDVTYLFARGTSEPGNVLVGPPLAEAFEGAVGASALSFQGVNG-YASAV-E 134
 QY 69 NFLPRGTQANIDEGKRLFALANQ-----KCPNTPVWAGGYSGAALIAAAVSELSGAV 122
 Db 135 GYLGG-----EAAGSKAMASQASDILSKCPDTKLVMSGYSGQCGIIVHNAVEQLPAEH 187
 QY 123 KEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSYTIETARG 182

```
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR FILING DATE: 1997-04-02
; PRIOR FILING DATE: 1997-04-02
; PRIOR FILING DATE: 1997-11-10
; PRIOR FILING DATE: 1997-11-10
; PRIOR FILING DATE: 1997-04-18
; PRIOR FILING DATE: 1997-04-18
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-14

Query Match 18.8%; Score 187.5; DB 10; Length 219;
Best Local Similarity 31.7%; Pred. No. 1.1e-11;
Matches 66; Conservative 32; Mismatches 75; Indels 35; Gaps 11;

QY 8 GLESGSANACPDAILIFARGSTEGPNNGITVGPALANGLSHI-RNIWIQGVGGPYDAAL 66
Db 25 GAVAPATAACPDAAEVVFARGFPFGIG-TVGNFVSALRSKVNKNVAVKYPAD--- 80

QY 67 ATNPLPGTQANIDEKRLFALANQKCPNTPVAVGYSOGAA---LIAAAVSELSGAVK 123
Db 81 --NQIDVGAN---DMSAHQISMAN-SCPNTRLVPGYSLGAAYTDVVLAVPTQMWGFTN 133

QY 124 -----EQVKGVALFGYTONLQNRGGP---RRTKVFNCVNGDAVCTGTLII--- 170
Db 134 PLPPGSDHEHTAVALFG--NGSQWVGPIITFNSPAYNDRTIELCHGDGDPVCHPADPNTWEA 191

QY 171 --PAHLSYTIIEARG---EAAARFLRDRI 193
Db 192 NWPHLAGAYVSSGMVNAQADFAVGKQ 219

RESULT 6
US-09-791-171-52
; Sequence 52, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-52

Query Match 16.8%; Score 167.5; DB 10; Length 262;
Best Local Similarity 32.1%; Pred. No. 1.5e-09;
Matches 68; Conservative 22; Mismatches 67; Indels 55; Gaps 13;

QY 14 ANACPDAILIFARGSTEGPNNGITVGPALANGLSHIRNIWIQGVG---GPYDAALATNF 70
Db 41 ADGCPDAEVTFARGTGPFGIG-RVGOAFVDSL------QQTGMGICGVYPVNAASR 91
QY 71 LP-RGTSQANIDEKRLFALANQKCPNTPVAVGYSOGAAL--IAAAV-----SELS 119
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; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-52

Query Match 17.9%; Score 179; DB 10; Length 226;
Best Local Similarity 32.5%; Pred. No. 8.4e-11;
Matches 63; Conservative 24; Mismatches 75; Indels 32; Gaps 11;

QY 17 CPDAILIFARGSTEGPNNGITVGPALANGLSHI-RNIWIQGVGGPYDAALATNPLPRGT 75
Db 47 CPDAEVVFARGTGPFGIG-RVGOAFVSSLRQQTINKSIGTYGVNYPANG---DFLAAD 101

QY 76 SQANIDEGKRLFALANQKCPNTPVAVGYSOGAA---LIAAA-----VSELSGAVKEQ 125
Db 102 GANDASDHIOQMASA---CRATRLVLGGYSOGAAVIDIVTAAPLPGGLGFTQPLPPAADH 158

QY 126 VKGVALFGYTONLQNRGG-----IPNYPRETRKVFNCVNGDAVCT-GTLIITPAHLSYTI 178
Db 159 IAAIALFG---NFSGRAGGLMSALTPOF-GSKTINLCNNGDPICSDGNNR--WRAHLGYVP 212

QY 179 EARGEAAARFLRDRI 192
Db 213 GMTNQAAARFVASRI 226

RESULT 7
US-09-791-171-56
; Sequence 56, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-56

Query Match 16.8%; Score 167.5; DB 10; Length 262;
Best Local Similarity 32.1%; Pred. No. 1.5e-09;
Matches 68; Conservative 22; Mismatches 67; Indels 55; Gaps 13;

QY 14 ANACPDAILIFARGSTEGPNNGITVGPALANGLSHIRNIWIQGVG---GPYDAALATNF 70
Db 41 ADGCPDAEVTFARGTGPFGIG-RVGOAFVDSL------QQTGMGICGVYPVNAASR 91
QY 71 LP-RGTSQANIDEKRLFALANQKCPNTPVAVGYSOGAAL--IAAAV-----SELS 119
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Db 92 LQHHGGDGAN-DAISHIKSNAS-SCNTKLVLGGYSQGTATVIVAGVPLGSIISFGSPLP 149
QY 120 GAVKEQVKGVALGYTONLNRGS-----IPNYPRTKVFNCVGDVACTGTLLITPAH 173
Db 150 AYADNVAAVAFG-----NPSNRAGGSLSLPLFGSKAIDL-CNTPDPIC-----H 196
QY 174 LSYTIEARG-----EAARFLRDRIRA 194
Db 197 VGPNEFSGHIDGYIPTTYTQRAASFVVQRLRA 228

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RESULT 8

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US-10-051-643-197
; Sequence 197, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 197
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-051-643-197

Query Match 14.5%; Score 145; DB 9; Length 285;
Best Local Similarity 28.6%; Pred. No. 3e-07;
Matches 60; Conservative 31; Mismatches 71; Indels 48; Gaps 14;

QY 9 LESGSANACPDAILIFARGG-TEPGNMGITVGPALANGLESIRNIWIQVGGPYDAALA 67
Db 27 IPTASADPCDIEVIFARGTGAEPG-LG-WGDAFVNALRPKVG----QSVG----TYA 76
QY 68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVGYSQGAALIAAAV--- 115
Db 77 VNYPAGFDFDKSAPMGAAAS---GRVQWMDN--CPDTKLVLGMSQAGVIDLITVDP 131
QY 116 -----SELGAVKEQVKVALGY-TQNLQNGGIPNYP---RERTKVFNCVGDVAVC 163
Db 132 RPLGRFTPTMPPRVADHVAAVVFGNPLRDIRGGGLPQMSGTYGPKSIDLCALDDDPFC 191
QY 164 TGTLLITPAHLSYNT---TEARGEAAFLR 189
Db 192 SPGFNL-FAHFAYANGMVE---EAANFAR 217

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RESULT 9

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US-10-051-643-154
; Sequence 154, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17

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; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 154
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (119)...(119)
US-10-051-643-154

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Query Match 11.9%; Score 119; DB 9; Length 748;
Best Local Similarity 31.1%; Pred. No. 0.00044;
Matches 51; Conservative 21; Mismatches 52; Indels 40; Gaps 12;

QY 9 LESGSANACPDAILIFARGG-TEPGNMGITVGPALANGLESIRNIWIQVGGPYDAALA 67
Db 27 IPTASADPCDIEVIFARGTGAEPG-LG-WGDAFVNALRPKVG----QSVG----TYA 76
QY 68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVGYSQGAALIAAAV--- 115
Db 77 VNYPAGFDFDKSAPMGAAAS---GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131
QY 116 -----SELGAVKEQVKVALGY-TQNLQNGGIPNYP-PR 149
Db 132 RPLGRFTPTMPPRVADHVAAVVFG--NPLRDIRGGGRLEPR 173

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RESULT 10

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US-10-051-643-112
; Sequence 112, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 112
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (119)...(119)
US-10-051-643-112

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Query Match 11.6%; Score 116; DB 9; Length 167;
Best Local Similarity 30.1%; Pred. No. 0.00013;
Matches 44; Conservative 19; Mismatches 47; Indels 36; Gaps 9;

QY 9 LESGSANACPDAILIFARGG-TEPGNMGITVGPALANGLESIRNIWIQVGGPYDAALA 67
Db 27 IPTASADPCDIEVIFARGTGAEPG-LG-WGDAFVNALRPKVG----QSVG----TYA 76
QY 68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVGYSQGAALIAAAV--- 115
Db 77 VNYPAGFDFDKSAPMGAAAS---GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131
QY 116 -----SELGAVKEQVKVALFG 133
Db 132 RPLGRFTPTMPPRVADHVAAVVFG 157

```


RESULT 14
US-09-738-626-6668

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: January 2, 2003, 15:04:24 ; Search time 20 Seconds
(without alignments)
932.504 Million cell updates/sec

Title: US-09-873-075A-1
Perfect score: 999
Sequence: 1 QIGAIENGLESGSANACPDA.....SYTIERGEAAARFURDRIRA 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 2832224

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	601.5	60.2	228	1	S20448	cutinase (EC 3.1.1.-	
2	584	58.5	224	1	B27451	cutinase (EC 3.1.1.-	
3	584	56.5	223	1	S21427	cutinase - fungus	
4	558.5	55.9	230	1	A27451	cutinase (EC 3.1.1.-	
5	553	55.4	228	1	UVFUS	cutinase (EC 3.1.1.-	
6	197.5	19.8	217	2	F70756	probable cutinase	
7	187.5	18.8	219	2	A70734	probable cutinase	
8	179	17.9	226	2	A70565	probable cutinase	
9	167.5	16.8	247	2	H70564	probable cutinase	
10	114.5	11.5	187	2	F70796	probable cutinase	
11	103	10.3	336	2	F70887	hypothetical prote	
12	98	9.8	174	2	G70987	probable cutinase	
13	95	9.5	336	2	C86921	conserved hypothet	
14	89	8.9	420	2	T35575	hypothetical prote	
15	89	8.9	592	1	S13391	endo-1,4-beta-xyla	
16	88.5	8.9	317	2	B82637	bifunctional bioti	
17	88.5	8.9	6486	2	T31076	tyrocidine synthet	
18	88	8.8	3535	2	S83641	probable hemagglut	
19	87	8.7	892	2	E76350	hypothetical prote	
20	86.5	8.7	123	2	B86656	hypothetical prote	
21	86.5	8.7	200	2	A69903	hypothetical prote	
22	86	8.6	357	2	A95190	hypothetical prote	
23	86	8.6	357	2	B98056	hypothetical prote	
24	86	8.6	5627	2	C83339	hypothetical prote	
25	84.5	8.5	302	2	S71334	acetyl xylan ester	
26	83.5	8.4	338	2	A83846	stage V sporulatio	
27	83.5	8.4	382	2	A87548	3-carboxy-cis,cis-	
28	83	8.3	1293	2	A90707	enterobactin synth	
29	83	8.3	1293	2	E85557	enterobactin synth	

30	83	8.3	1356	2	T18521	beta transducin-l1
31	83	8.3	8563	2	T30226	polyketide synthet
32	82.5	8.3	398	2	D83214	conserved hypothet
33	82.5	8.3	665	2	F37032	beta-glucosidase f
34	82.5	8.3	685	2	F37032	beta-glucosidase f
35	82	8.2	329	2	T30289	pristinamycin I sy
36	82	8.2	329	2	B46678	endoglycosidase F3
37	81	8.1	260	2	H84116	hypothetical prote
38	81	8.1	380	2	C83618	probable CoA trans
39	80	8.0	466	2	B70544	probable histidino
40	79.5	8.0	459	2	J02263	glutamate-l-semial
41	79.5	8.0	749	2	T36334	hypothetical prote
42	79.5	8.0	2082	2	E95889	probable dehydroge
43	79	7.9	442	2	T37056	probable multi-dom
44	79	7.9	462	2	A52917	carboxy-terminal p
45	78.5	7.9	243	2	H97691	carboxy-terminal p
					A11049	probable tRNA/rRNA

ALIGNMENTS

RESULT 1
S20448
cutinase (EC 3.1.-.-) - rice blast fungus
C:Species: Magnaporthe grisea (rice blast fungus)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S20448
R:Swiegard, J.A.; Chumley, F.G.; Valent, B.
Mol. Gen. Genet. 232, 174-182, 1992
A:Title: Cloning and analysis of CUT1, a cutinase gene from Magnaporthe grisea.
A:Reference number: S20448; MJID:92212279; PMID:1557023
A:Accession: S20448
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-228 <SWE>
A:Cross-references: GB:X61500; NID:g9298; PIDN:CAA43717.1; PID:g1045205
C:Genetics:
A:Gene: Cut1
C:Superfamily: cutinase
C:Keywords: hydrolase

Query Match	60.2%;	Score	601.5;	DB	1;	Length	228;	
Best Local Similarity	60.0%;	Pred. No.	1.6e-45;					
Matches	117;	Conservative	27;	Mismatches	50;	Indels	1;	
Gaps	1;							
QY	1	QLGAIENGLESGSANACPDALII	FARGSTPCNNGITVGPALANG	LESHRN-TWIOGVG	59			
Db	33	QLNSVRNDLISGNAACP	SVLII	PARASGEVNGLSAGT	VNSKLEREF	RNDI	WQGVG 92	
QY	60	GPYDAAALATNPLPGT	TSOANTIDEGKRUF	FALANQKCPNT	FPVVAGGY	SGQAALIAA	VSLS 119	
Db	93	DPYDAALSPNLF	PAGTTQGAIDEAKRFT	LANTKCPNAA	VVAGGY	SGQTAFVNF	AVSEMP 152	
QY	120	GAYKEOVKGVALFCYT	ONLQNRGGI	PKNP	PRERTKVC	NGVDACVTG	TLLITPAHLSY	179
Db	153	AAVODQIKGVVFL	FGYTKNLQNRGRIP	DPFTEKTE	YVICNASD	AVCGTLL	FLPAHFLY	212
QY	180	ARGEAAARFL	DRIRA	194				
Db	213	SSIAAPNWL	IROIRA	227				

RESULT 2
B27451 precursor - anthracnose fungus (Colletotrichum gloeosporium) (EC 3.1.-.-)
C:Species: Glomerella cingulata, Colletotrichum gloeosporioides
C:date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 03-Mar-1994
C:Accession: B27451
R:Rittering, W.F.; Thukral, S.K.; Kolattukudy, P.E.
Biochemistry 26, 7883-7892, 1987
A:Title: Structure of cutinase gene, cDNA, and the derived amino acid sequence
A:Reference number: A90524
A:Accession: B27451

R;Lin, T.S.; Kolattukudy, P.E.
Eur. J. Biochem. 106, 341-351, 1980
A:Title: Structural studies on cutinase, a glycoprotein containing novel amino acids and
A:Reference number: A44665; MUID:80245930; PMID:7398618
A:Contents: annotation; identification of glucuronylated amino end
C:Comment: This enzyme catalyzes the hydrolysis of cutin, a polyester that forms the str
C:Genetics: Southern blot results suggest that the genome contains two copies of the cuti

A:Introns: 64/3
A:Superfamily: cutinase
C:Keywords: blocked amino end; glycoprotein; hydrolase
F:1-31/domain: signal sequence #status predicted <SIG>
F:32-230/Product: cutinase #status predicted <MAT>
F:32/Modified site: glucuronylated amino end (Gly) (in mature form) #status experimental
F:125-187/Disulfide bonds: #status experimental
F:136,204/Active site: Ser, His #status experimental

Query Match 55.4%; Score 553; DB 1; Length 230;
Best Local Similarity 55.3%; Pred. No. 3e-41;
Matches 109; Conservative 32; Mismatches 52; Indels 4; Gaps 3;

QY 1 QLG-ATENGLEGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHT--RNTWIOG 57
Db 30 QLGRTRDDLLINGSACRDIYIYARGSTETGNLG-TLGFSTASNLESFAGDKGVWIOG 88
QY 58 VGGPYDAALATNPLRGTQANIDECKRLFPALANQKCPNTPVVGYSOGAALIAAAYSE 117
Db 89 VGGAYRATLGDNALPRTGSAAREMLGLFQQANTKCPDATLIGGYSOGAALAAASIED 148
QY 118 LSGAVKEQVKGVALFGYTONLQNRGIPNTPRRTKVFNCVNGDAVCTGTLIIIPAHLSYT 177
Db 149 LDSAIRDKIAGTVLFGYTKNLQNRGIPNTPADRTKVFNCVNGDAVCTGTLIIIPAHLSYT 208

QY 178 IEARGEAREFLDRIRA 194
Db 209 PDARGPAPEFLIEKIRA 225

RESULT 6
F70756
probable cutinase precursor with N-terminal signal sequence - Mycobacterium tuberculosis
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70756

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70756

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-217 <COL>
A:Cross-references: GB:Z74025; GB:AL123456; NID:93261586; PIDN:CAA98399.1; PID:g1403471
A:Experimental source: strain H37Rv
C:Genetics: Rv1984c
C:Superfamily: cutinase

Query Match 19.8%; Score 197.5; DB 2; Length 217;
Best Local Similarity 30.8%; Pred. No. 4.7e-10;
Matches 61; Conservative 26; Mismatches 88; Indels 23; Gaps 7;

QY 8 GLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTNRTWIOGVGPDAAAL 67
Db 26 GGRAAHADPCDIIVFARGTHOASGLG-DVGEAFVDSLTQSQ-----VGGRSIGVYA 76
QY 68 TNFLP-----RGTQANIDECKRLFPALANQKCPNTPVVGYSOGAALIAAAYSELSGAVK 123
Db 77 VNPASDDYASASNGSDDASAHQRTVASCNPTRIVLGGYSOGATVIDLSTAMPAPVA 136

QY 124 EOYKGVALF-----GYTONLQNRGIPNYP---RERTKVFNCVNGDAVCTGTLIIIPAHLS 175
Db 137 DHVAALVAFGEPSGSSGSSMLGSGSLPTIGLYSSKTINLCAPDDPICTGGNIM-AHVS 195
QY 176 YTIEA-RGEAARFLDRIR 192
Db 196 YVQSGMTSQAATFAANRL 213

RESULT 7
A70734
probable cutinase precursor - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: A70734

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70734

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-219 <COL>
A:Cross-references: GB:Z77163; GB:AL123456; NID:93261610; PIDN:CAB00997.1; PID:g14493
A:Experimental source: strain H37Rv
C:Genetics: A70734
C:Superfamily: cutinase

Query Match 18.8%; Score 187.5; DB 2; Length 219;
Best Local Similarity 31.7%; Pred. No. 3.6e-09;
Matches 66; Conservative 32; Mismatches 75; Indels 35; Gaps 11;

QY 8 GLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHT--RNTWIOGVGPDAAAL 66
Db 25 GAVAPATAACPDAAEVVFARGSTPEGNMGITVGPALANGLESHT--RNTWIOGVGPDAAAL 80
QY 67 ATNPLRGTQANIDECKRLFPALANQKCPNTPVVGYSOGAA---LIAAAYSELSGAVK 123
Db 81 --NQIDVGAN---DMSAHTQSMAN-SCPNTRLVPGYSGLGAATDVVLVAPVTQMMGFTN 133
QY 124 -----EQVKGVALFGYTONLQNRGIPNYP---RERTKVFNCVNGDAVCTGTLII--- 170
Db 134 PLPPGSDERHTAAVALFG--NGSOWVGPITNFPSPAYNDRITIELCHGDDPVCHPADPNTWEA 191
QY 171 --PAHLSYITEARG---EAARFLDRIR 193
Db 192 NWPQHLGAGAYVSSGMVNNQAADFVAGKLIQ 219

RESULT 8
A70565
probable cutinase precursor - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: A70565

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70565

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-226 <COL>
A:Cross-references: GB:Z95390; GB:AL123456; NID:93261766; PIDN:CAB08718.1; PID:g21043
A:Experimental source: strain H37Rv
C:Genetics: A70565

A:Gene: RV3452
C:Superfamily: cutinase

Query Match
Best Local Similarity 17.9%; Score 179; DB 2; Length 226;
Matches 63; Conservative 24; Mismatches 75; Indels 32; Gaps 11;

QY 17 CPDAILFARGSTPGNMGITVGPALANGLESRI-RNIWIOGVGGPYDAALATNFILPRGT 75
|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 47 CPDAEVVFARGTGPPGLG-RVGQAFFVSRLRQTNKSGTGYGVNPANG----DFLAAAD 101
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 76 SQANIDGKRLFALANKCPNTVPVAGYSOGAA---LIAA-----VSELSGAVKEQ 125
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 102 GANDASDHIIQQMASA---CRATRVLGGYSOGAAVIDIVTAAPLPGLGTQPLPPAADH 158
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 126 VKGVALFGYTQNLRNGG-----IPNYPRRTKVFCNVGDVACT--GTLIINPAHLSYTI 178
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 159 IAAIALEFG---NPSGRAGGLMSALTPOF-GSKTINLCNNGDPICSGDNR--WRAHLGYYP 212
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 179 EARGEARAFLRDRI 192
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 213 GMTNQARFVASRI 226
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9
H70564
probable cutinase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: H70564
C:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; PMID:98295987; PMID:9634230
A:Accession: H70564
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-247 <COL>
A:Cross-references: GB:Z95390; GB:AL123456; NID:g3261766; PIDN:CAB08717.1; PID:g2104374
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV3451
C:Superfamily: cutinase

Query Match
Best Local Similarity 16.8%; Score 167.5; DB 2; Length 247;
Matches 68; Conservative 22; Mismatches 67; Indels 55; Gaps 13;

QY 14 ANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIQGVG---GPYDAALATNF 70
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 26 AGCCPDAEVTFARCTGEPPGIG-RVGAQFVDSLr-----QQTGMEIGVYPVVAASR 76
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 71 LP-RGTSQANIDEGKRLFALANKCPNTVPVAGYSOGAAL--IAAAV-----SELS 119
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 77 LQLHGDDGAN-DAISHIKSMAS-SCPNTKLVLGGYSOGATVIDIVAGVPLGSISFGSPLP 134
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 120 GAVKEOVKGVALFGYTQNLRNGG-----IPNTPRETKVFCNVGDVACTGTLIITPAH 173
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 135 AYADNVAAVAVERG---NPSNRAGGSLSSLPFGSKAIDL-CNPDTDPIC-----H 181
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 174 LSVYTEARG-----EAAERFLDRIRA 194
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 182 VCGPNEFSCHIDGIPTTYTTQAASFVVQRURA 213
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
E70796
Probable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: E70796
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A: Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A: Reference number: A70500; MUID: 98295987; PMID: 9634230
A: Accession: E70796
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-187 <COL>
A: Cross-references: GB:AL022121; GB:AL123456; NID: g3261559; PIDN: CAA18046.1; PID: g296
A: Experimental source: strain H37Rv
C: Genetics:
A: Gene: Rv3724
C: Superfamily: cutinase

Query Match 11.5%; Score 114.5; DB 2; Length 187;
Best Local Similarity 26.4%; Pred. No. 0.0078;
Matches 43; Conservative 22; Mismatches 75; Indels 23; Gaps 6;

QY 51 RNIWIOGVGPYDAALATNLFPRGTSQANIDEGKRLFLANOKCPNTPVVAGGYSQGAAL 110
DB 27 KSLGVTVAVNPASNDPFSSDPFKTVIDIGIRDAGSHISMA-MSCPQTRVLGGYSQGA 85
QY 111 -----IAAAVSELSGAVKEQVKGVALFG--YTQNLQNRGGIP----NYPRE 150
DB 86 AGVTVSAVVPVPPVQAVPAPMAPEVANHVAAVTLFGAPSAQFLGQYGAPPIATGPLYQP 145
QY 151 RRVKFCNVGDVACTGTLITPAHLSYTIEAR-GEAARFLRDRI 192
DB 146 KTLQLCADGDSIC-GDGNSPVAHGLYAVNGVGGGANFAASRL 187

RESULT 11
F70887
hypothetical protein Rv3802c - Mycobacterium tuberculosis (strain H37Rv)
C: Species: Mycobacterium tuberculosis
C: Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C: Accession: F70887
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A: Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A: Reference number: A70500; MUID: 98295987; PMID: 9634230
A: Accession: F70887
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-336 <COL>
A: Cross-references: GB:AL022076; GB:AL123456; NID: g3256026; PIDN: CAA17866.1; PID: e125
A: Experimental source: strain H37Rv
C: Genetics:
A: Gene: Rv3802c

Query Match 10.3%; Score 103; DB 2; Length 336;
Best Local Similarity 22.7%; Pred. No. 0.16;
Matches 50; Conservative 24; Mismatches 86; Indels 60; Gaps 9;

QY 16 ACPDALLIFARGSTE-----PGNMGITV-GPALANGLESHIRNIWIOGVGGP 61
DB 71 SCPDVQMSVPGTWSSPQNPLNPVQFFKALLKVTGPITAQQAPARVOTYTVAYTAQF 130
QY 62 YDAALATNLFPRGTSQANIDEGKRLFLA-----NQRCPNTPVVAGGYSQGAALIAAAV 117
DB 131 HNPLTTDQMSYNSDRA---EGTRAMVAATMDNNRCPLTSYVLIGFSQGAIVAGDVASD 187
QY 118 LS---GAVKEQ-VKGVALFGYTNLQNRGG-IPNYPR----- 149
DB 188 TGNRGQVDEDLVLGVTLLADRGROGVGNQVPPSPRGEGAEITLHEVPVLSGLIGLTMGT 247

QY 150 -----ERTKVCNVGDVCTG-TLITPAHLSYTI 178
 Db 248 PRPGFGALDGRNEICAOGLDCAAPQAFAFSPANLPTTL 287

RESULT 12
 G70987
 probable cutinase - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: G70987
 R:Colet, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: G70987
 A:Molecule type: DNA
 A:Residues: 1-174 <COL>
 A:Cross-references: GB:Z95890; GB:AL123456; NID:g3242245; PIDN:CAB09321.1; PID:g2131026
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: Rv1758
 C:Superfamily: cutinase

Query Match 9.8%; Score 98; DB 2; Length 174;
 Best Local Similarity 29.9%; Pred. No. 0.2;
 Matches 52; Conservative 22; Mismatches 64; Indels 36; Gaps 12;

QY 44 NGLESHT--RNIIQTGVGGPYDAALATNPLRGTSQANI-DEGKRLFALANOKCPNTPVV 100
 Db 11 DALRSKIGESMGVGVDP-----ATTDEP--TAMAGIYDATHVEQTA-ANCPQSKLV 62

QY 101 AGYSOGAALI-----AAVSE-----LSGAVKEQVKGVALFGY--TQNLRNGGIP 145
 Db 63 LGGFSOGAAVMGFVTAAPADGAPLADPRMPPEVADHVAATLFGMPVSFAFMHSIGAPP 122

QY 146 ----NYPRETKVFCNVGDVCT--GTLITPAHLSYTIARGE--RARFLRDRI 192
 Db 123 IVIGPLYAEKTIQLCAPGDPVCSGGN---WAAHNGYADDMVEQAFAAAGRL 173

RESULT 13
 C86921
 conserved hypothetical protein ML0099 [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: C86921
 R:Colet, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holroyd, S.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Massive gene decay in the leprosy bacillus.
 A:Reference number: A86909; MUID:21128732; PMID:11234002
 A:Accession: C86921
 A:Molecule type: DNA
 A:Residues: 1-336 <STO>
 A:Cross-references: GB:AL450380; NID:g13092481; PIDN:CAC29607.1; GSPDB:GN00147
 C:Genetics:
 A:Gene: ML0099

Query Match 9.5%; Score 95; DB 2; Length 336;
 Best Local Similarity 22.5%; Pred. No. 0.79;
 Matches 53; Conservative 19; Mismatches 86; Indels 78; Gaps 11;

QY 16 ACPDAILLIARGSTEG-----NNGITVGPALANGLESHIRNIQGV 58
 Db 71 SCPDVLVVVPGRWESSLODNLPLDPYQFPDALLRNSTWTIGQQFPT---SRVQTYTI--- 124

QY 59 GGPYDAALATNPLRGTSQANID-----EGKRLEAL-----ANOKCPNTPVVAGYSOGAAL 110
 Db 125 --PYTAQFHNPL--SGDKQMTYNDRAEGTRAMVQEMINVNKCPLTSTYVLVFGSOGAVI 180

QY 111 IAAVSELS---GAVKEQ-VKGVVALFGYTONLRNGI---PNYPRE----- 150
 Db 181 AGDITSDIGNHGHPVDDDLVGLVTLIADRRQOQGVGNDIGPNPPGEGAEVTLHEVPVLSG 240

QY 151 -----RTKVCNVGDVCTG-----TLITPAHLSYTIARGE 183
 Db 241 LGMTWTGARPGGFGVLHSTRNEICAPGDLICAAPAEAFSVANLPTLNTLASGAGQ 296

RESULT 14
 T35575
 hypothetical protein SC6G4.24 SC6G4.24 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C:Accession: T35575
 R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1998
 A:Reference number: Z21583
 A:Accession: T35575
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-420 <SAU>
 A:Cross-references: EMBL:AL031317; PIDN:CAA20402.1; GSPDB:GN00070; SCOEDB:SC6G4.24
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC6G4.24

Query Match 8.9%; Score 89; DB 2; Length 420;
 Best Local Similarity 26.9%; Pred. No. 3.4;
 Matches 36; Conservative 20; Mismatches 64; Indels 14; Gaps 5;

QY 10 EGSANACPDAILIFARGSTEGPNTGMITVGPALAN-----GLESHIRNI-WIQGVGG 60
 Db 105 EAG-ADPAPRRRLFGKAPAPVTVFVSHGYCLNQDSWHFQRAALRGVRSVYWDQRSHG 163

QY 61 PYDAALATNPLRGTSQANIDE-GKRLFALANOKCPNTPVVAGYSOGAALIAAVSELS 119
 Db 164 RSGRGVAQT---RDDRPRVSTEEELGRDLKAVIDAAAPGPTVLGVSHSGMGTVMALADAFP 220

QY 120 GAVKEQVKGVALFG 133
 Db 221 DLVRERVGVGVALVG 234

RESULT 15
 S13391
 endo-1,4-beta-xylanase (EC 3.2.1.8) B - Pseudomonas fluorescens subsp. cellulosa
 N:Alternate names: xylanase B
 C:Species: Pseudomonas fluorescens subsp. cellulosa
 C:Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 18-Jun-1999
 C:Accession: S13391
 R:Kelllett, L.E.; Poole, D.M.; Ferreira, L.M.A.; Durrant, A.J.; Hazlewood, G.P.; Gilbe, Biochem. J. 272, 369-376, 1990
 A>Title: Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens subsp. cellulosa
 A:Reference number: S13391; MUID:91097447; PMID:2125205
 A:Accession: S13391
 A:Molecule type: DNA
 A:Residues: 1-592 <KEL>
 A:Cross-references: EMBL:X54523; NID:g45523; PIDN:CAA38389.1; PID:g45524
 C:Genetics:
 A:Gene: xynB
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
 A:Pathway: xylan degradation
 C:Superfamily: Pseudomonas endo-1,4-beta-xylanase B; bacterial cellulose-binding domain
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:38-134/Domain: bacterial cellulose-binding domain homology <BCB>
 F:337-592/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>

F:39-133/Disulfide bonds: #status predicted
F:431/530/Active site: Glu #status predicted

Query Match	8.9%	Score 89;	DB 1;	Length 592;
Best Local Similarity	24.9%	Pred. No. 5.1;		
Matches 43;	Conservative 19;	Mismatches 69;	Indels 42;	Gaps 8;

QY	15	NACPDAILIFARGSTEPGNNGITVGPALANGLESIRNIWIOGVGGPY-DAAL-----	66
Db	378	NNIPVKAHTFVWGAQSPSNLNLSPPEVAVEIQ-----WIRDYCARYPDTAMIDVVNEA	432
QY	67	ATNFLPRGTSQANIDEG--KRLFALANQKCPNTPPVVAGY-----SQGAA	109
Db	433	VPGHQPGAGYAQRAFGNNWIQRVFQLARQYCPNSILILNDYNNIRWQHNEFIALAKAQGN	492
QY	110	LIAAAVVS--ELSGAVKEQVKGVAFQYTONLONRGGIPNYPRERTKVCNVD	160
Db	493	IDAVGLQAHKLGMTAAQVKA-----IDNIWQVKGKPIYISE-----YDIGD	535

Search completed: January 2, 2003, 15:06:43
Job time : 21 secs


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FT ACT_SITE 191 191 BY SIMILARITY.
FT ACT_SITE 204 204 BY SIMILARITY.
SQ SEQUENCE 224 AA; 23477 MW; 1C5BACEAB469AFA CRC64;

Query Match 58.58; Score 584; DB 1; Length 224;
Best Local Similarity 59.08; Pred. No. 9.4e-43;
Matches 111; Conservative 28; Mismatches 47; Indels 2; Gaps 1;

QY 7 NGLSSGANACPDAILIFARGSTPGNMGITVGPALANGLES--HIRNIWIOGVGGPYDA 64
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 36 NELETGSSACPVIYIFARASTEPGNMGISAGPIVADALERIYICANNVWQGVGGPYLA 95
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 65 ALATNPLPGTSONIDEGKRLFLANOKCPNTPVWAGYSQGAALIAAAVSELSGAVKE 124
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 96 DLASNFLPDGTSSAINEARLFTLANCKPNAIIISVGGYSQGTAVMAGSISGLSTTIKN 155
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 125 QVKGVALFGYTONLQNGGIPNYPRTKVCNVDGAVCTGLTIITPAHLSYTIARGE 184
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 156 QIKGVVLFGYTKNLQNGRIPNFTSKVTEYCDIADAVCYGTLFILPAHFLYQDAVAA 215
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 185 ARFLRDRI 192
   ||: ||
Db 216 PRFLQARI 223

RESULT 4
CUTI_ASCRA
ID CUTI_ASCRA STANDARD; PRT; 223 AA.
AC P2922;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUT.
OS Ascochyta rabiei.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC mitosporic Pezizomycotina; Ascochyta.
OX NCBI_TaxID=5454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CBS 534.65;
RA Tenhaken R., Barz W.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection (By similarity).
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O -> cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By contact with cutin.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
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CC -----
CC EMBL; X65628; CAA46582.1; -
CC PIR; S21427; S21427.
CC HSP; P00590; ICWU.
CC InterPro; IPR000675; Cutinase.
CC Pfam; PF01083; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC Hydrolase; Serine esterase; Signal.
KW SIGNAL 1 19
FT CHAIN 20 223
FT DISULFID 46 192 BY SIMILARITY.
FT 124 185
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FT ACT_SITE 135 135 BY SIMILARITY.
FT ACT_SITE 189 189 BY SIMILARITY.
FT ACT_SITE 202 202 BY SIMILARITY.
SQ SEQUENCE 223 AA; 23520 MW; 1E82A5ADD1B5E7FB CRC64;

Query Match 56.58; Score 564; DB 1; Length 223;
Best Local Similarity 58.68; Pred. No. 4.7e-41;
Matches 112; Conservative 29; Mismatches 48; Indels 2; Gaps 2;

QY 5 IENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLES--IRNIWIOGVGGPYD 63
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 34 IRSELEGGSSCKAILIFARGSTPGNMGISAGPAVASALEAYGADQIIVWQGVGGPYT 93
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 64 AALATNPLPGTSONIDEGKRLFLANOKCPNTPVWAGYSQGAALIAAAVSELSGAVK 123
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 94 ADLPSNFLPGTSSAINEARLFTLANCKPNAIIISVGGYSQGTAVMAGIAPKLD-AYR 152
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 124 EQVKGVALFGYTONLQNGGIPNYPRTKVCNVDGAVCTGLTIITPAHLSYTIARGE 183
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 153 ARVGVTLFGYTONQNNKGIDKYPQEDLQVYCEVGDVCDGLTIITVSHFLYLEEAAGP 212
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 184 AARELDRIRA 194
   ||: ||
Db 213 APEFLKSKIGA 223

RESULT 5
CUTI_COLCA
ID CUTI_COLCA STANDARD; PRT; 228 AA.
AC P10951;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUTA.
OS Colletotrichum capsici (Anthracnose fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC mitosporic Phyllachoraceae; Colletotrichum.
OX NCBI_TaxID=5456;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 48574;
RA Ettinger W.F., Thukral S.K., Kolattukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid
RT sequence from phytopathogenic fungi.";
RL Biochemistry 26:7883-7892(1987).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O -> cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By contact with cutin.
CC -!- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CC CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
CC BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M18033; AAA33043.1; -
CC PIR; A27451; A27451.
CC HSP; P00590; ICWU.
CC InterPro; IPR000675; Cutinase.
CC Pfam; PF01083; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
```

DR PROSITE: PS00155; CUTINASE_1; 1.
 DR PROSITE: PS00931; CUTINASE_2; 1.
 KW Hydrolyase; Serine esterase; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 228
 FT DISULFID 49 198
 FT ACT_SITE 129 191
 FT ACT_SITE 140 140
 FT ACT_SITE 195 195
 FT ACT_SITE 208 208
 SQ SEQUENCE 228 AA; 23714 MW; 3825D42C23DA139B CRC64;

Query Match 55.9%; Score 558.5; DB 1; Length 228;
 Best Local Similarity 57.7%; Pred. No. 1.4e-40;
 Matches 109; Conservative 27; Mismatches 50; Indels 3; Gaps 2;

QY 7 NGLSGSANACPDAILIFARGSTPCNMGITVGPALANGLESH--IRNIWIOGVGGPYDA 64
 Db 39 NELESGSSNCPKVIIFARASTPCNMGISAGPIVADALESRYGASQVWVGQVGGPYSA 98
 QY 65 ALATNF-LPRGTSQANIDEKRLFLANOKPNTVPVAGGYSGQAALIAAAVSELGAVK 123
 Db 99 DLASNFIIPEGTSRAINEAKRLFTLANTKCPNSAVVAGGYSGQTAVMASSISELSSTIQ 158
 QY 124 EOYKGVALFYTONLQNRGIPNYPRRTKVFNCVGDVACTGTLITPAHLSTIARGE 183
 Db 159 NQIKGVVLSAITKNLQNLGRIPNFTSKTEVYCALADAVCYGTLFLPAHFLYQADAATS 218
 QY 184 AARFLRDRI 192
 Db 219 APFLAARI 227

RESULT 6
 CUTI_FUSSC
 ID CUTI_FUSSC STANDARD; PRT; 230 AA.
 AC Q99174:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cutinase precursor (EC 3.1.1.74).
 GN CUTA.
 OS Fusarium solani (subsp. cucurbitae) (Nectria ipomoeae).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Nectriaceae; Nectria.
 OX NCBI_TaxID=571162;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PGB 153;
 RX MEDLINE=97254598; PubMed=9100380;
 RA Crowhurst R.N., Binnie S.J., Bowen J.K., Hawthorne B.T., Plummer K.M.,
 RA Rees-George J., Rikkerink E.H., Templeton M.D.;
 RT "Effect of disruption of a cutinase gene (cutA), on virulence and
 RT tissue specificity of Fusarium solani f. sp. cucurbitae race 2 toward
 RT Cucurbita maxima and C. moschata".
 RL Mol. Plant Microbe Interact. 10:355-368(1997).
 CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
 CC forms the structure of plant cuticle. Allows pathogenic fungi to
 CC penetrate through the cuticular barrier into the host plant during
 CC the initial stage of the fungal infection.
 CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.

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 CC -----
 DR EMBL; U63335; AAB05922.1; "

DR HSSP: P00590; 2CUT.
 DR InterPro: IPR000675; Cutinase.
 DR Pfam: PF01083; Cutinase; 1.
 DR PRINTS: PR00129; CUTINASE.
 DR PROSITE: PS00155; CUTINASE_1; 1.
 DR PROSITE: PS00931; CUTINASE_2; 1.
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 230
 FT DISULFID 47 194
 FT ACT_SITE 125 187
 FT ACT_SITE 136 136
 FT ACT_SITE 191 191
 FT ACT_SITE 204 204
 SQ SEQUENCE 230 AA; 23902 MW; 05FB3C33326405AA CRC64;

Query Match 55.9%; Score 558; DB 1; Length 230;
 Best Local Similarity 55.8%; Pred. No. 1.6e-40;
 Matches 110; Conservative 32; Mismatches 51; Indels 4; Gaps 3;

QY 1 QLGL-ALNGLSGSANACPDAILIFARGSTPCNMGITVGPALANGLESHI--RNWIOG 57
 Db 30 QLGRITRDDLINGNSASCADVIFIYARGSTETGNLG-TLGPSTIASNLESFAGTGDGVWIOG 88
 QY 58 VGGPYDAALATNPLPRGTSQANIDEKRLFLANOKPNTVPVAGGYSGQAALIAAAVSE 117
 Db 89 VGGVATRLTGDNALPRGTSAAIREMLGLFQQAOKCPDATTIAGGYSGQAALAAASIED 148
 QY 118 LSCAVKEQYKGVALFYTONLQNRGIPNYPRRTKVFNCVGDVACTGTLITPAHLST 177
 Db 149 LDSAINDKIAGTVLFGYTKNLQNRGIPNYPADRTKVFNCVGDVCTGLSIIAAPHLAYG 208
 QY 178 IEARGEAAARFLRDRI 194
 Db 209 PDARGPAPEFLIEKVRA 225

RESULT 7
 CUTI_FUSSO
 ID CUTI_FUSSO STANDARD; PRT; 230 AA.
 AC P00590:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cutinase 1 precursor (EC 3.1.1.74).
 GN CUTI OR CUTA.
 OS Fusarium solani (subsp. pisi) (Nectria haematococca).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Nectriaceae; Nectria.
 OX NCBI_TaxID=70791;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-T-8;
 RA Soliday C.L., Flurkey W.H., Okita T.W., Kolattukudy P.E.;
 RT "Cloning and structure determination of cDNA for cutinase, an enzyme
 RT involved in fungal penetration of plants".
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3939-3943(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8917761; PubMed=2703464;
 RA Soliday C.L., Dickman M.B., Kolattukudy P.E.;
 RT "Structure of the cutinase gene and detection of promoter activity in
 RT the 5'-flanking region by fungal transformation".
 RL J. Bacteriol. 171:1942-1951(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=92220194; PubMed=3560844;
 RA Martinez C., de Geus P., Lauwereys M., Matthysens G., Cambillau C.;
 RT "Fusarium solani cutinase is a lipolytic enzyme with a catalytic
 RT serine accessible to solvent".
 RL Nature 356:615-618(1992).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

Handwritten notes:
 F-
 cutin

Query Match 18.8%; Score 187.5; DB 1; Length 219;

TIGR; WT3557;	-
DR Tuberculist; RV3451;	-
DR InterPro; IPR000675; Cutinase.	
DR Pfam; PF01083; Cutinase; 1.	
DR PROSITE; PS00155; CUTINASE_1.	1.
DR PROSITE; PS00931; CUTINASE_2; FALSE_NEG.	
KW Hypothetical protein; Hydrolase; Serine esterase; Signal;	
KW Complete proteome.	
SIGNAL	1
FT CHAIN	26
FT FT	27
FT DISULFID	29
FT FT	99
FT ACT_SITE	110
FT FT	177
FT ACT_SITE	191
FT FT	22
FT CONFLICT	194
FT KW	SEQUENCE
FT FT	247 AA;
FT SQ	24884 MW; 07B04671A056D5FF CRC64;
Query Match	16.88; Score 167.5; DB 1; Length 247;
Best Local Similarity	32.18; Pred. No. 2.4e-07;
Matches	68; Conservative 22; Mismatches 67; Indels 55; Gaps 13;
QY 14 ANACPDAILIFARGSTPEPGNGITVGPALANGLESHRNWIQGVG---	GYPDAALATNF 70
DB 26 ADGPCDAEVTFARGTGGPPGIG-RVGQAFVDLSR-----	QQTGMGIVPVPNYAASR 76
QY 71 LP-RGTSQAINDCKRLFALANQRCPNTPPVAGYSQGAAL--IAAAV-	-----SELS 119
DB 77 LQLHGGGAN-DALSHIKSMAS-SCPNKTLVLGYSGCATVIDIVAGVPLGSISFGSPLP	134
QY 120 GAVKEQVKGVAFGYTONLNRGG-----IPNPTRRTKVCNVGDVAVCTGLTIITPAH	173
DB 135 AAYADNTAAVAVFV---NPSNRAGSSLSPLFLGSKAIDL-CNPTDPIC-----	H 181
QY 174 LSytiEARG-----EAARFLRDRIIRA 194	
DB 182 VGPNEFSGHIDGIPIYTTOQASFVVORLRA 213	
RESULT 15	
ID XYNB_PSEFL	
AC XYNB_PSEFL	STANDARD; PRF: 592 AA.
ID P23030;	
DT 01-NOV-1991 (Rel. 20, Created)	
DT 01-NOV-1991 (Rel. 20, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)	
DE (1,4-beta-D-xylan xylanohydrolase B).	
GN XYNB.	
OS Pseudomonas fluorescens.	
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	
OC Pseudomonas.	
OX NCBI_TaxID=294;	
[]	
RN SEQUENCE FROM N.A., AND SEQUENCE OF 39-56.	
RY STRAIN=Sp. Cellulosa;	
RX MEDLINE=61097447; PubMed=2125205;	
RA Kellett L.E., Poole D.M., Ferreira L.M.A., Durrant A.J.,	
RA Hazlewood G.P., Gilbert H.J.;	
RT "Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens	
RT subspp. cellulosa contain identical cellulose-binding domains and are	
RT encoded by adjacent genes."	
RL Biochem. J. 272:369-376(1990).	
CC -! FUNCTION: XYLANASE B CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE	
CC MAJOR COMPONENT OF PLANT CELL-WALLS..	
CC -! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic	
CC linkages in xyans.	
CC -! PATHWAY: Hemicellulose degradation.	
CC -! SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL	
CC HYDROLASES).	
CC -! SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN	
CC (CBD).	

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X54523; CAA38389.1; -.
DR PIR; S13391; S13391.
DR HSSP; P07986; LEXG.
DR InterPro; IPR001919; Bac_cellose-band.
DR InterPro; IPR001000; Glyco_hydro_10.
DR Pfam; PF00331; Glyco_hydro_10; 1.
DR Pfam; PF00553; CBM_2; 1.
DR PRINTS; PR00134; GLHYDRLASE10.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE; PS00561; CBD_BACTERIAL; 1.
KW Cellulose degradation; Xylan degradation; Hydrolase; Glycosidase;
KW Signal.
FT SIGNAL 1 38
FT CHAIN 39 592
FT DOMAIN 39 134 ENDO-1,4-BETA-XYLANASE B.
FT DOMAIN 135 160 CELLULOSE-BINDING (BY SIMILARITY).
FT DOMAIN 300 320 SER-RICH (LINKER).
FT ACT_SITE 431 431 SER-RICH (LINKER).
FT ACT_SITE 431 431 PROTON-DONOR (BY SIMILARITY).
FT ACT_SITE 530 530 NUCLEOPHILE (BY SIMILARITY).
FT DISULFID 39 133 BY SIMILARITY.
SQ SEQUENCE 592 AA; 63410 MW; E081F6308EA2B93A CRC64;

Query Match 8.9%; Score 89; DB 1; Length 592;
Best Local Similarity 24.9%; Pred No. 2.8;
Matches 43; Conservative 19; Mismatches 69; Indels 42; Gaps 8;

QY 15 NACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIQGVGGPY-DAAL----- 66
Db 378 NNIPVKAHTFVWGAQSPSWLNLGSGPEVAVEIEQ-----WIRDYCARYPDTAMIDVVNEA 432
QY 67 ATNPLPGTTSQANIDEG--KRLFALANQKCPNTPVVGYY-----SQGAA 109
Db 433 VPGHOPAGYAQAFAGNNWTFQRFQALQYCPNLSILINDYNNIRWQHNEFIALAKAQGY 492
QY 110 LIAAAVS--ELSGAVKEQVKGVALFGYTONLQNRGIGPNYPRRTKVFNCVGD 160
Db 493 IDAVGLQAHELAGMTAAQVKTA-----IDNIWNVGKPIYISE-----YDIGD 535

Search completed: January 2, 2003, 15:05:39
Job time : 13 secs

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.: "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).

[2]

SEQUENCE FROM N.A.

RA STRAIN=CDC 1551 / OSHKOSH;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

RA Peterson J., Deboy R., Dodson R., Gwinn M., Haft D., Hickey E.,

RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

RA Delcher A.F., Utterback T., Weidman J.J., Khouri H., Gill J., Mikula A.,

RA Bishai W.;

RA "Whole genome comparison of Mycobacterium tuberculosis clinical and

RA laboratory strains.";

RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z95390; CAB08718.1; ALT_INIT.

DR EMBL; AE007160; AAK47898.1; -.

DR HSSP; P00590; ICUZ.

DR TIGR; MT3559; -.

DR TubercuList; Rv3452; -.

DR InterPro; IPR000675; Cutinase.

DR InterPro; IPR000379; Ser_estrs_site.

DR Pfam; PF01083; Cutinase; 1.

DR KW Hypothetical protein; Complete proteome.

DR SEQUENCE 231 AA; 23686 MW; 45943C6B23FPB480 CRC64;

Query Match 17.98; Score 179; DB 16; Length 231;

Best Local Similarity 32.5%; Pred. No. 3.8e-07;

Matches 63; Conservative 24; Mismatches 75; Indels 32; Gaps 11;

QY 17 CPDAILIFARGSTPGNGMITVGPALANGLESHI-RNIWIOGVGGPYDAALATNPLPRGT 75

DB 52 CPDREVFPARTGEPGLG-RVGAQFVSSLRQOTNKSIGTVGVNYPANG-----DFLAAAD 106

QY 76 SQANIDEKRLFALANOKPNTVPVAGYSOGAA---LIAAA-----VSELSGAVKEQ 125

DB 107 GANDASDHQOMASA---CRATRLVLGGYSOGAAVIDIVTAAPLPLGLFTQPLPPAADH 163

QY 126 VKGVALLFGYTONLQNRGG-----IPNYPRETKVFCNVGDVACT-GTLITPAHLSYTI 178

DB 164 IAAALTFG---NPSGRAGGLMSALTPOF-GSKTINLCNNGDPICSDGNR--WRAHLGYVP 217

QY 179 EARGEAAFLRDR 192

DB 218 GMTNQARFVASRI 231

RESULT 7

Q9KK87 PRELIMINARY; PRT; 220 AA.

AC Q9KK87;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Serine esterase cutinase.

OS Mycobacterium avium.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_Taxid=1764;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=969A45; TISSUE=BLOOD;

RA Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.;

RT "Identification of Mycobacterium avium DNA sequences that encode

RT exported proteins by using phoA gene fusions.";

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF139058; AAF74988.1; -.

DR InterPro; IPR000675; Cutinase.

DR InterPro; IPR000379; Ser_estrs_site.

DR Pfam; PF01083; Cutinase; 1.

DR PROSITE; PS00155; CUTINASE_1; 1.

```
DR PROSITE, PS00931; CUTINASE_2; UNKNOWN_1.
SQ SEQUENCE 220 AA; 22394 MW; CBF49F47FF65D9C CRC64;

Query Match 16.1%; Score 160.5; DB 2; Length 220;
Best Local Similarity 28.1%; Pred. No. 1.2e-05;
Matches 54; Conservative 35; Mismatches 82; Indels 21; Gaps 8;

QY 13 SANACPDAILIFARGSTEGPNNIGTVGPALANGLSHI--RNIIQGVGGPYDAALATNF 70
DB 31 AADPGSDVVFARGTHOBPGILG-NIGQAFVDSLTSQLGSRSDVYVAVNYP-----AND 83
QY 71 LPRGTSQANIDGKRLFLALANQKCPNTPVWAGYSQGAALIAAAVSELSGAYKEQVKGYA 130
DB 84 DYHNSANAGADASAHVQDTVAACPSNRSLVGLGYSQGSTVIDLATNAMPSPVADHVAAYA 143
QY 131 LF-----GYTONLQNRGNIPNYP---RERTKFCVNGVQAVCTGLIITPAHLSYTYEA-- 180
DB 144 LFGEPSSGFSTLMWGQPLPTINPLYGKGTISLCAPDDPICSGGNGIM-AHVSY-IDAGM 201
QY 181 RGEARFLRDRI 192
DB 202 TAAQAATFAANHL 213

RESULT 8
Q9XB09 PRELIMINARY; PRT; 143 AA.
AC Q9XB09;
DT 01-NOV-1999 (TremBLrel. 12, Created)
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE RVD2-RV1758 (fragment).
GN RVD2-RV1758.
OS Mycobacterium bovis BCG.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=33892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCG-PASTEUR; PubMed=10320585;
RX MEDLINE=99255698; PubMed=10320585;
RA Gordon S.V., Brosch R., Billault A., Garnier T., Eiglmeyer K.,
RA Cole S.T.;
RT "Identification of variable regions in the genomes of tubercle bacilli
RT using bacterial artificial chromosome arrays."
RL Mol. Microbiol. 32:643-655(1999).
DR EMBL; Y18606; CAB44660.1; -.
DR HSSP; P00590; 1XZJ.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 14434 MW; 6CBA62B8174755E7 CRC64;

Query Match 13.2%; Score 132; DB 2; Length 143;
Best Local Similarity 36.6%; Pred. No. 0.0016;
Matches 41; Conservative 19; Mismatches 36; Indels 16; Gaps 7;

QY 13 SANACPDAILIFARGSTEGPNNIGTVGPALANGLSHI--RNIIQGVGGPYDAALATNF 70
DB 25 SDGACPDVEVVFARGTGPPGVG-GIGEDFDALRSKIGKSGMVGVDYP-----ATTD 78
QY 71 LPRGTSQANI-DEGKRLFLALANQKCPNTPVWAGYSQGAALI-----AAAVSE 117
DB 79 FP--TAMAGIVDAGTHVQTA-ANCPQSKLVGLGFSQGAAYGVFTAAAIPT 127

RESULT 9
O69691 PRELIMINARY; PRT; 207 AA.
AC O69691;
DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
```

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DE Putative cutinase precursor (Serine esterase, cutinase family).
GN RV3724 OR MT3827 OR MTV025.072.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022121; CAA18046.1; ALT_INIT.
DR EMBL; AE007179; AAK48196.1; -.
DR TIGR; MT3827; -.
DR TubercuList; RV3724; -.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
KW Complete proteome.
SQ SEQUENCE 207 AA; 21225 MW; 967510FD7C49D7D5 CRC64;

Query Match 11.5%; Score 114.5; DB 16; Length 207;
Best Local Similarity 26.4%; Pred. No. 0.071;
Matches 43; Conservative 22; Mismatches 75; Indels 23; Gaps 6;

QY 51 RNIIQGVGGPYDAALATNLPRTGSQANIDGKRLFLALANQKCPNTPVWAGYSQGAAL 110
DB 47 KSLGVYAVNYPASNDFASDDPKTVIDGIRDAGSHIQSMA-MSCPQTRQVLGGYSQGA 105
QY 111 -----TAAAVSELSGAYKEQVKGVALLFG--YTQNLRNGGIP----NYPRE 150
DB 106 AGYVTSVAVPPAVPQVAPPAPEVAVNVAATLFGASQAFQGLGQYGAIPGLYQP 165
QY 151 RTKVPNCNVGDAVCTGLIITPAHLSYTYEAR-GEAARFLRDRI 192
DB 166 KTLQLCADGDSIC-GDGNSPVAGHLYAVNGVMVGOGANFAASRL 207

RESULT 10
O59893 PRELIMINARY; PRT; 234 AA.
AC O59893;
DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Acetyl xylan esterase II (EC 3.1.1.6).
GN AXE-2.
OS Penicillium purpogenum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiota; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=28575;
RN [1]
RP SEQUENCE FROM N.A.
```

RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."		
RL	Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AL0202076; CAA17866.1; -		
DR	EMBL; AE0071184; AAK48275.1; -		
DR	TIGR; MT3909; -		
DR	TubercuList; RV3802c; -		
KW	Hypothetical protein; Complete proteome.		
SQ	SEQUENCE 336 AA; 35448 MW; F374D163449C6547 CRC64;		
	Query Match	10.3%;	Score 103; DB 16; Length 336;
	Best Local Similarity	22.7%;	Pred. NO. 1.1;
	Matches	50; Conservative	24; Mismatches 86; Indels 60; Gaps
QY	16	ACPDAILIFARGSTE-----	-PNNMGITV-GPALANGLESHIRNTWIOGVGP 61
Db	71	SCPDMQVMSIPGTSWESPOQNLPNVQFPKALLKVTGPIAQQFAPARVQTTVYTAQF 130	
QY	62	YDAALATNFUPRGTSQANTIDEGKRLEFALA----	NOKCPNTVPVAGYSOGAALIAAAVSE 117
Db	131	HNPLETDMQSYNDSRA---EGTRAMVAMTDMNRCPLTSVVLGFSGAVIAGDVASD 187	
QY	118	LS---GAVKEQ-YKGVALFGYTQNLQNRG-IPNYP-----	----- 149
Db	188	IGNRGVGDVDELVLGVTLLIADGRROQGVNOVPPSPRGSGAEITLHEVPVLISGLGLTWGT 247	
QY	150	-----ERTKVFCNVGDVACTG-TLLIITPAHLSYTI 178	
Db	248	PRGFGGALDRNEICAGDGLICAAPQAQFSPANLPTTL 287	
RESULT 12			
006793	ID	006793	PRELIMINARY; PRT; 174 AA.
AC	Q06793		
DT	01-JUL-1997	(TrEMBLrel. 04, Created)	
DT	01-JUL-1997	(TrEMBLrel. 04, Last sequence update)	
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)	
DE	Hypothesized 17.9 kDa protein (Serine esterase, cutinase family).		
GN	RV1758 OR WPCV29.24 OR WT1805.		
OS	Mycobacterium tuberculosis		
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;		
OC	Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.		
ON	NCBI_TaxID=1773;		
OX	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=H37RV;		
EX	MEDLINE=98295987; PubMed=9634230;		
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;		
RT	"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."		
RL	Nature 393:537-544(1998).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CDC 1551 / OSHKOSH;		
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;		
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."		
RL	Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; Z95890; CAB09321.1; -		
DR	EMBL; AE007040; AAK46078.1; -		
DR	HSSP; P00590.1; CIII		

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DR TIGR; MT1805; --
DR Tuberculin; Rv1758; --
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 174 AA; 17868 MW; 36684DEB29AE73C8 CRC64;

Query Match          9.8%; Score 98; DB 16; Length 174;
Best Local Similarity 29.9%; Pred. No. 1.3;
Matches 52; Conservative 22; Mismatches 64; Indels 36; Gaps 12;

Qy 44 NGLSHI--RNIIWIOGVGPGYDAALATNPLRGTSQANI-DEGKRLFALANQKCPNTVPV 100
Db 11 DALRSKIGKSGMVGVDYP-----ATTDFP--TAMAGIYDAGTHVEQTA-ANCPQSKLV 62

Qy 101 AGGYSGQAALI-----AAAVSE-----LSGAVKEQVKGVALFGY--TONLQNRGGIP 145
Db 63 LGGFSGQAAGVGFVTAALPDGAPLDAPRPPEVADHVAATLFGMFSVAFMHISIGAPP 122

Qy 146 ----NYPRTKVFNCVGDVCT--GTLIIIPAHLSTYEARGE--AARFLRDRI 192
Db 123 IVIGPLAETKTIQLCAPDGPVCCSGN---WAAHNGYADDMGVEQAFAAGRL 173

RESULT 13
ID Q9CDB3 PRELIMINARY; PRT; 336 AA.
AC Q9CDB3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE Hypothetical protein ML0099.
GN Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher T., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lactowix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; AL583917; CAC29607.1; --
DR Leproma; ML0099; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 336 AA; 35610 MW; 2D3B58AB526F633 CRC64;

Query Match          9.5%; Score 95; DB 16; Length 336;
Best Local Similarity 22.5%; Pred. No. 5.2;
Matches 53; Conservative 19; Mismatches 86; Indels 78; Gaps 11;

Qy 16 ACPDAILFARGSTEPG-----NMGITVGPALANGLESIRNIWIOGV 58
Db 71 SCPDVQLLVPGTWESSLQDNPLDPVOPDALLRNSTMTIGQFPF---SRVQYTI--- 124

Qy 59 GGPYDAALATNPLRGTSQANID---EGKRLFAL-----ANQKCPNTVPVAGYSQNAL 110
Db 125 --PYTAQFHNPL--SGDKQMTYNSRAGEGTRAMVQEMINVNKCPLTSLVLVGFSGQAVI 180

Qy 111 IAAAVSELS---GAVKEQ-VKGVALFGYTONLQNRGGI--PNYPRE----- 150
Db 181 AGDITSIGNHGHPVDDDLVLGVTLIADGRQOQGVNDIGNPPEGAEVTLHEVPVLGS 240
```

```
Qy 151 -----RTKVFNCVGDVCTG-----TLIIIPAHLSTYEARGE 183
Db 241 LGMVTGARGPGFGVLSHRTNEICAPGDLICAAPAEAFSVANPLATNLASGAGQ 296

RESULT 14
ID O30349 PRELIMINARY; PRT; 559 AA.
AC O30349;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE PEHR.
GN Pehr.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K60;
RX MEDLINE=98052122; PubMed=9390420;
RA Allen C., Gay J., Simon-Buela L.;
RT "A regulatory locus, pemsR, controls polygalacturonase production and
RT other virulence functions in Ralstonia solanacearum.";
RL Mol. Plant Microbe Interact. 10:1054-1064(1997).
CC -1- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
CC DOMAIN.
DR EMBL; AF001171; AAC24599.1; --
DR HSSP; P41789; INTR.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR002078; Sig54_interact.
DR Pfam; PF02954; HTH_8; 1.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00158; Sigma54_activat; 1.
DR PRINTS; PR01590; HTHFIS.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00448; REC; 1.
DR TIGRfams; TIGR01199; HTH_fis; 1.
DR PROSITE; PS00676; SIGMA54_INTERACT_2; UNKNOWN_1.
DR PROSITE; PS00045; SIGMA54_INTERACT_4; 1.
KW ATP-binding; DNA-binding; Phosphorylation; Sensory transduction;
KW Transcription regulation.
SQ SEQUENCE 559 AA; 60070 MW; 531BD5E392B558F9 CRC64;

Query Match          9.2%; Score 91.5; DB 2; Length 559;
Best Local Similarity 26.4%; Pred. No. 19;
Matches 55; Conservative 26; Mismatches 88; Indels 39; Gaps 11;

Qy 11 SGSNACPDAILIFARGSTEPGNMGITVG--PALANGLE-SHIRNIWIOGV----- 59
Db 75 SATADRTFPAV-ITAYGSAENAVEALKAGAFDYIAKPLSLDLRLSLNALGROQRDPDP 133

Qy 60 GPYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTVPVAGYSQAAALIAAVSELS 119
Db 134 GSADLAERTNALLPCHSAAMQEVRSLLRLARSMAV--VVISGSGSGKERAARIALHS 191

Qy 120 -----GAVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTG 167
Db 192 ARSPRFVAVNCAIPENLMEAEFFGV-----KGAFGTGADSDRQGF-----QAAHGTL 242

Qy 168 IITP-AHLSYTIARGEARELRD-RIR 193
Db 243 MLDEVADLPMTQVK--LLRLQDGRVR 268

RESULT 15
ID Q8TYQ4 PRELIMINARY; PRT; 455 AA.
AC Q8TYQ4;
```



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DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Asp-TRNAasn/Glu-trNAGin amidotransferase A subunit.
GN GATA OR MK0238.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyrii; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL: AE010321; AAC01455.1; ...
KW Transferase; Complete proteome.
SQ SEQUENCE 455 AA; 48829 MW; A0BE405605EAA7B7 CRC64;

Query Match 9.0%; Score 90; DB 17; Length 455;
Best Local Similarity 26.7%; Pred. No. 19;
Matches 43; Conservative 20; Mismatches 58; Indels 40; Gaps 10;

QY 18 PDA-ILIFARGST--EPGNMGITVGPALA-----NGLESHIRNIWIGVGGPYDAALA 67
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 32 PDINALIYINGGAPEEVGSEGLAGVAIAVKANINVEGMPDCASKTLEGYRAPFDATVV 91
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 68 TNFLPRGTSQ---ANIDEGKRLPALA-----NOKCPNTPVVGYSQG-AALI 111
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 92 RRIKEAGAAVIGIANMDE---FAAGSSGETSCHGPTDNPFCPR--IPGSSSGSAAAV 145
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 112 AAAY-----SELGAVKEQVK--GVALFGYTQNLQNRGGI 144
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 146 AAGLCDALGSDYGGSIKRNPAHCGVVGFKPTTYGLVPRQGL 186
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

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Search completed: January 2, 2003, 15:06:17
Job time : 32 secs

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